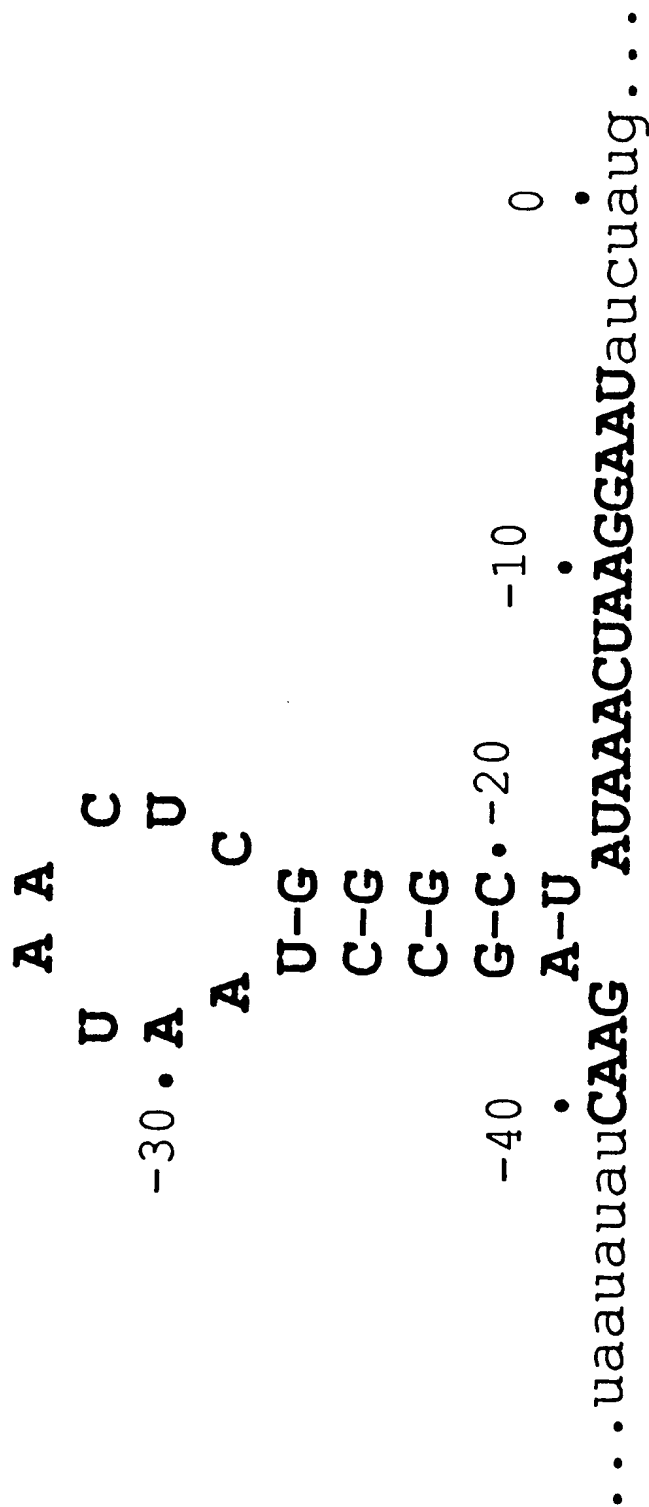


FIG. I



SEQ. I.D. NO. 345

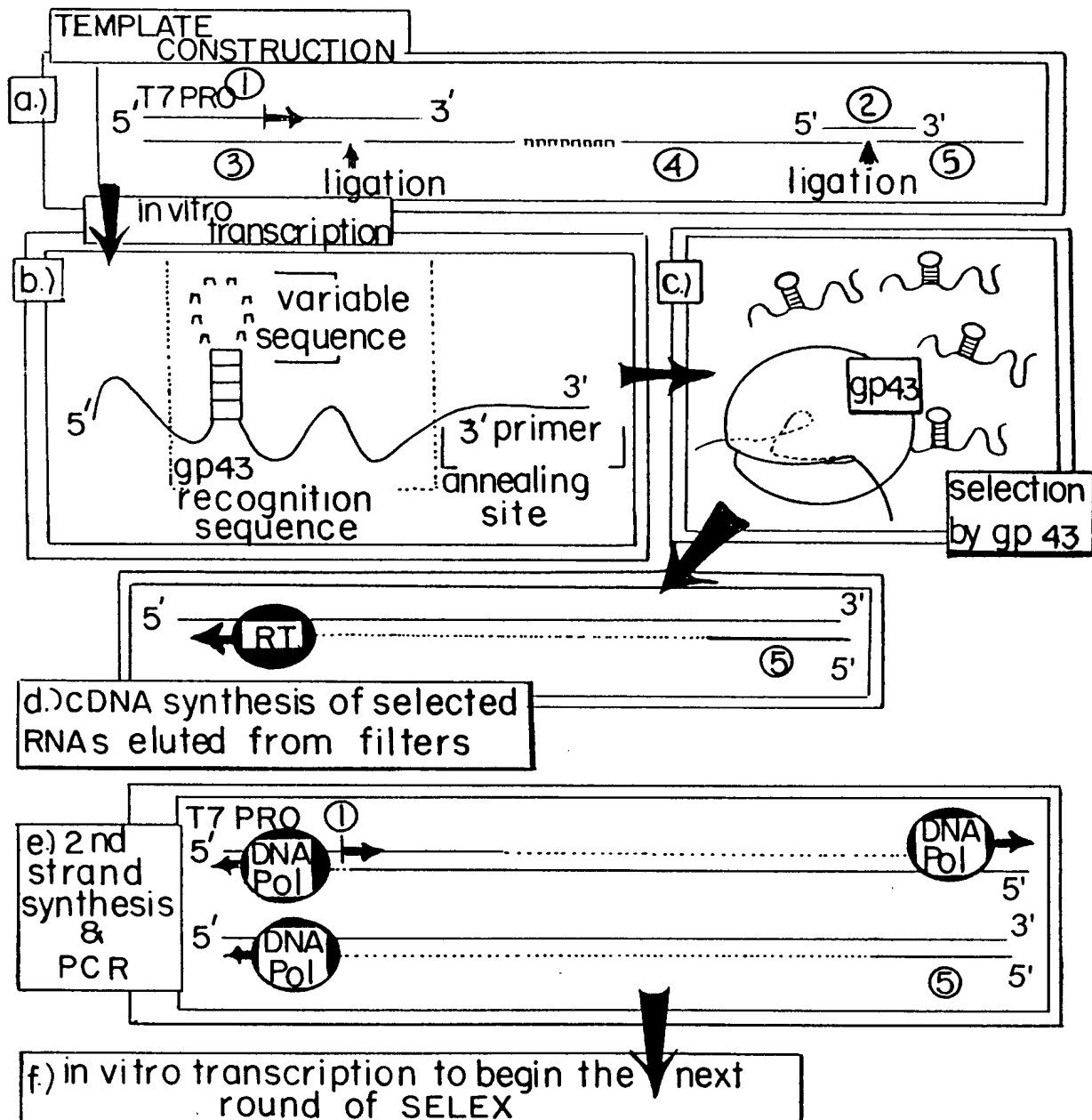


FIG.2

FIG. 3

SELECTION CYCLE:

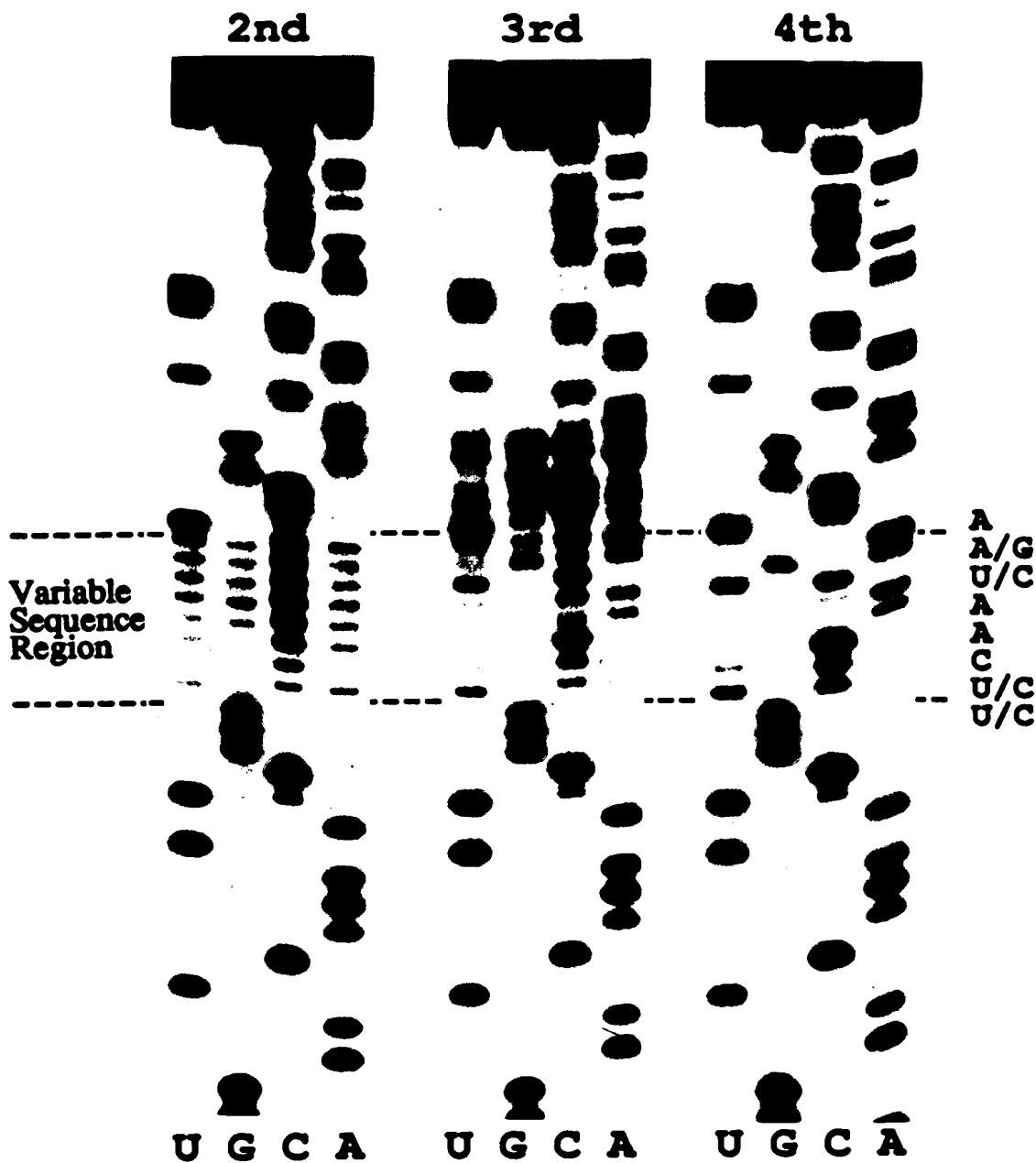
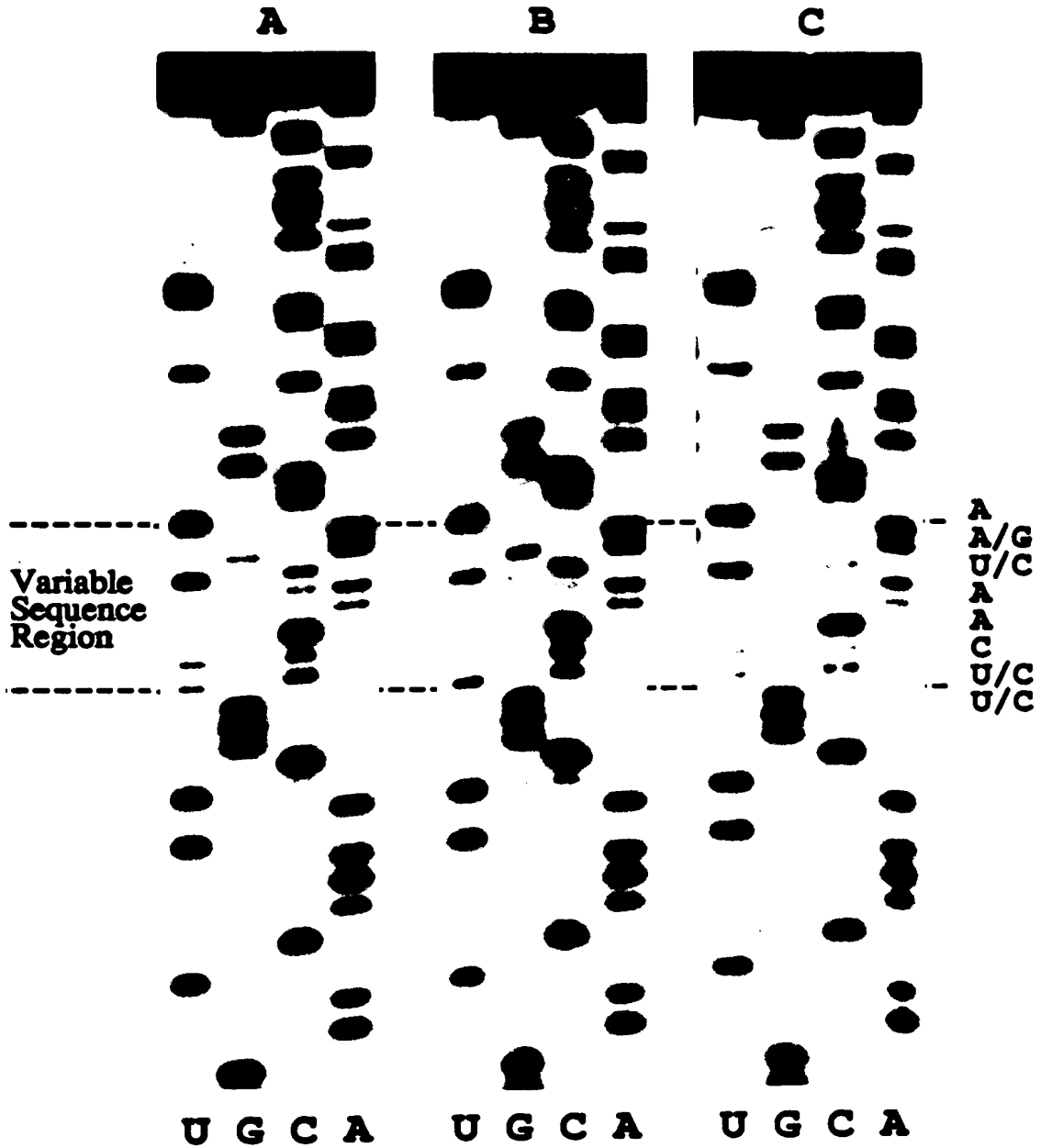


FIG. 4

EXPERIMENT:



40037906-101501

FIG. 5

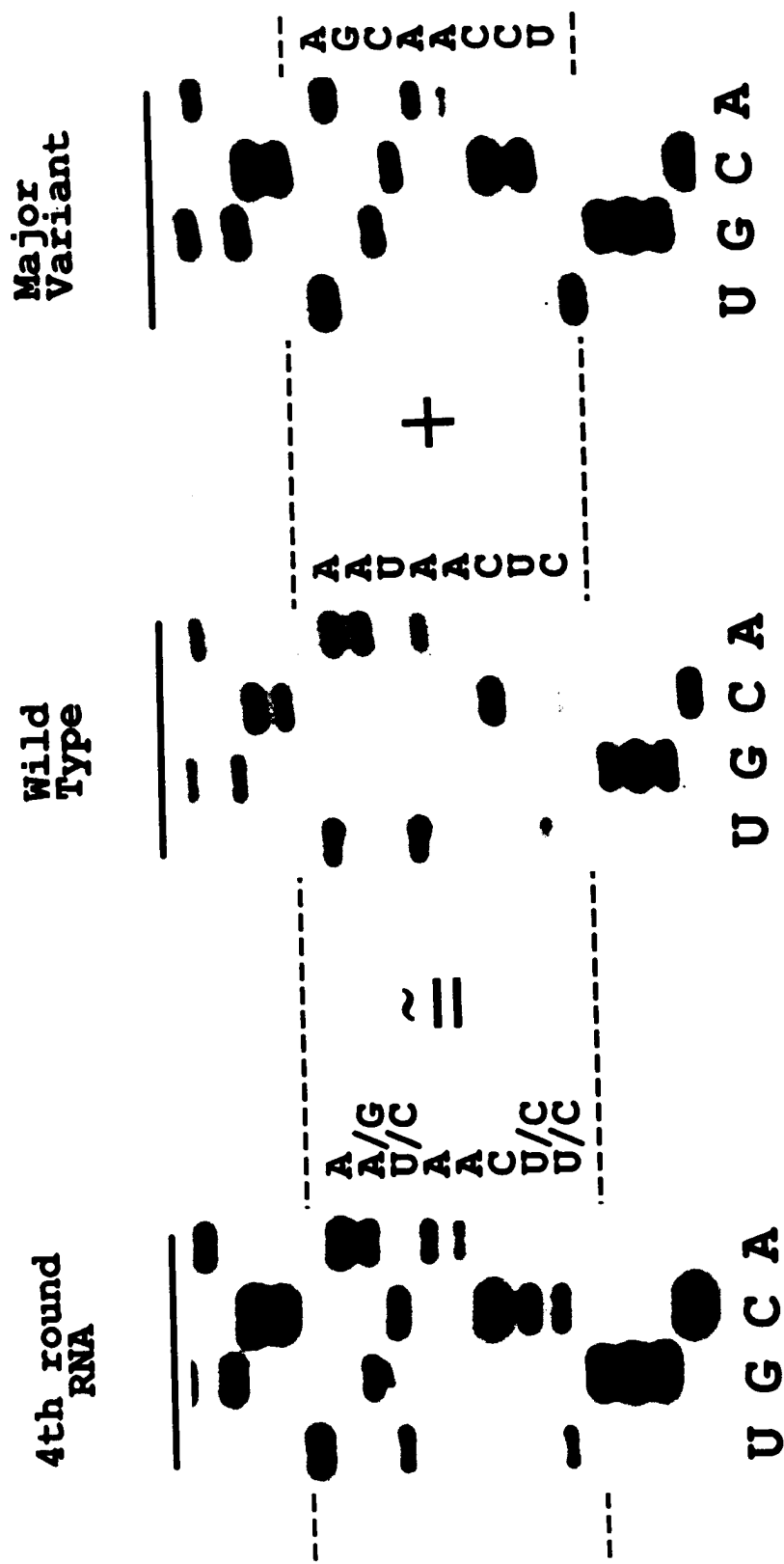
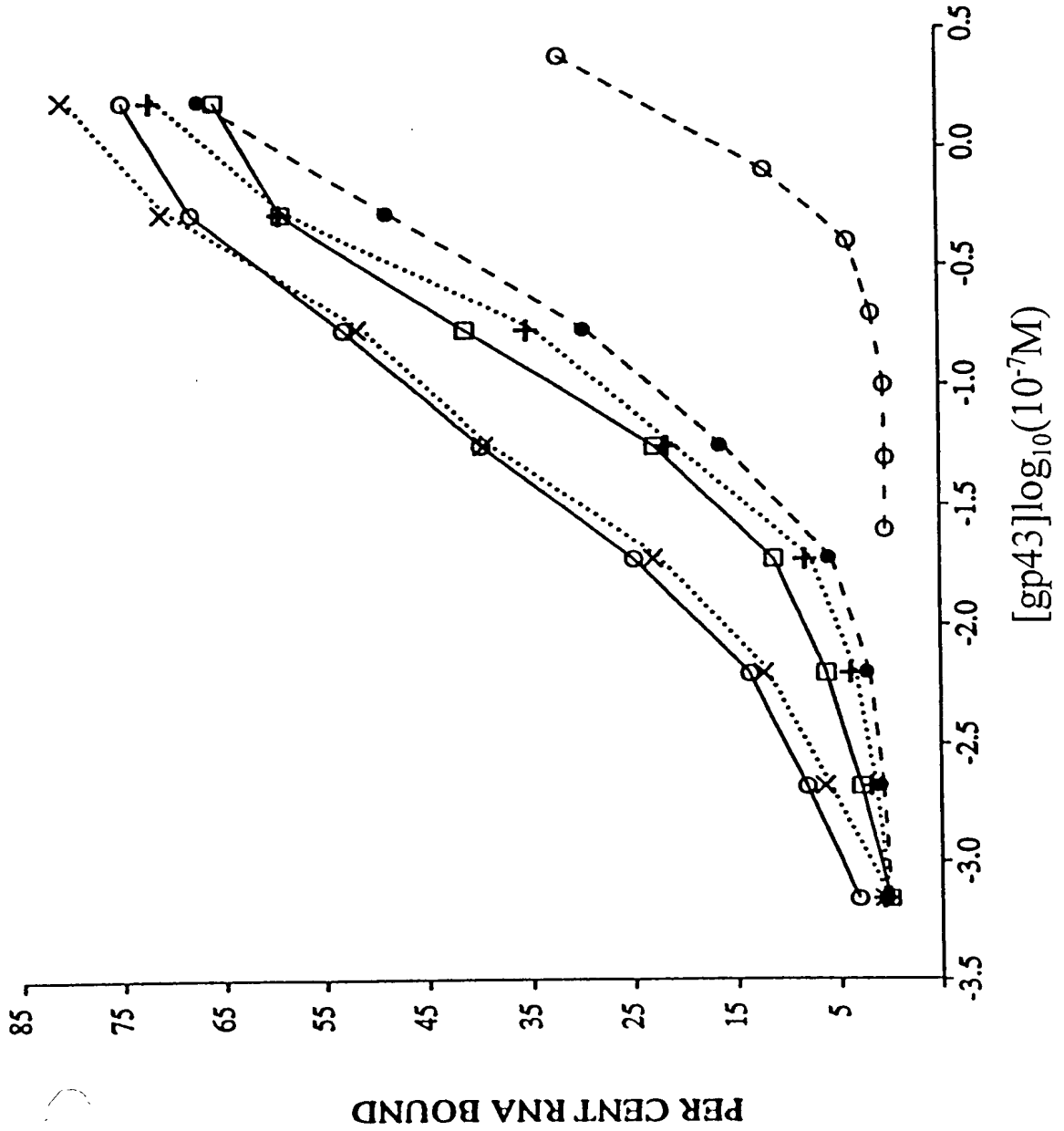


FIG. 6



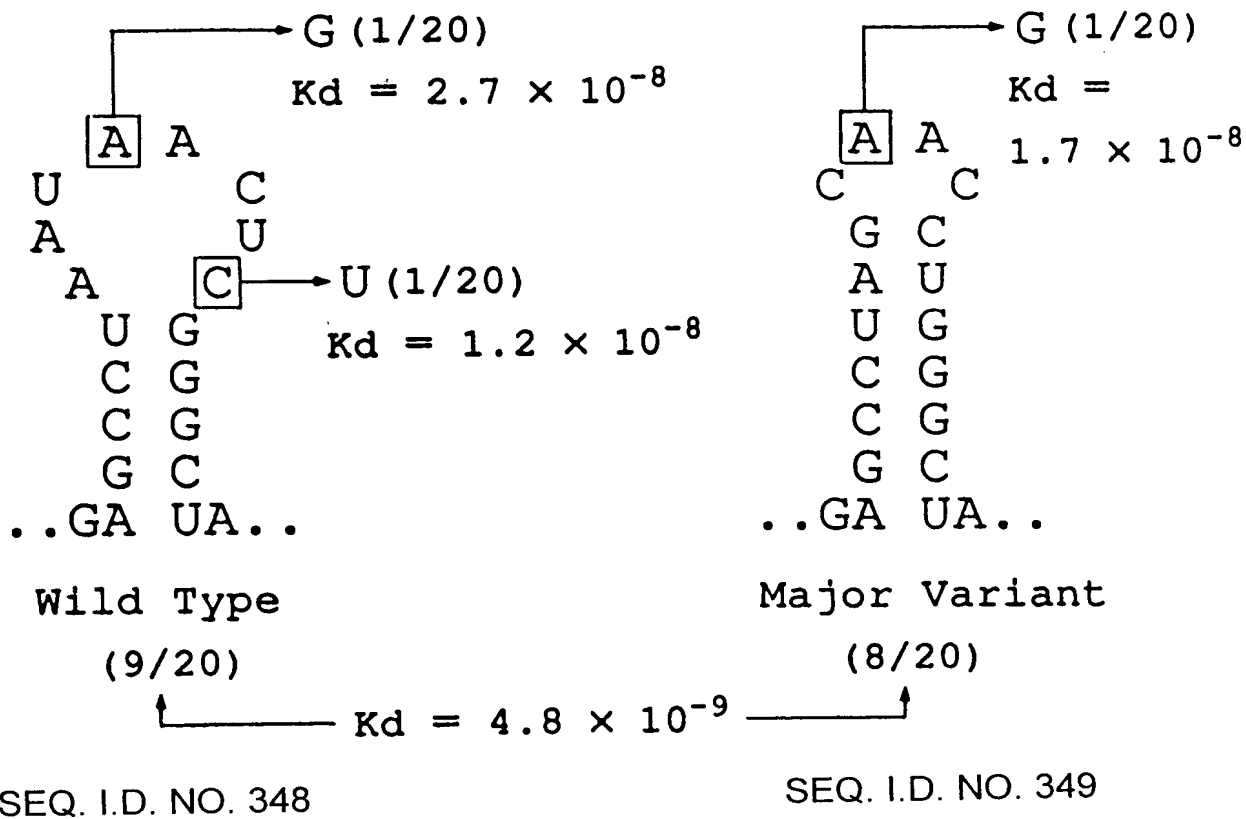
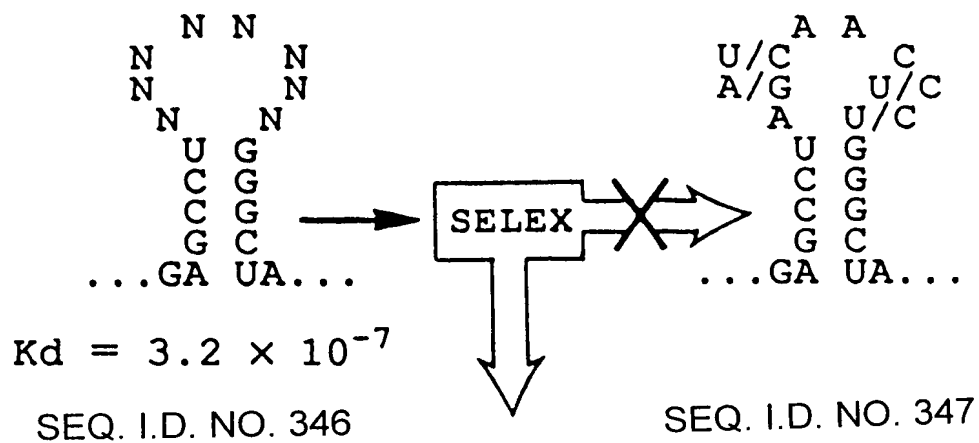


FIG. 7

# VARIABLE TEMPLATE SYNTHESIS USING TERMINAL TRANSFERASE

5' PRIMER  
 (OR PRIMARY LIGAND SEQUENCE) 3' 3' PRIMER 5'

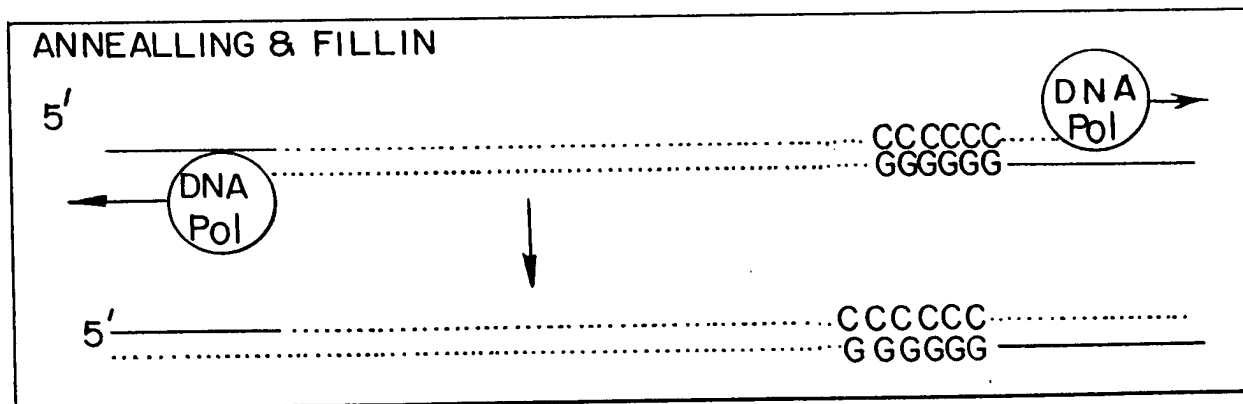
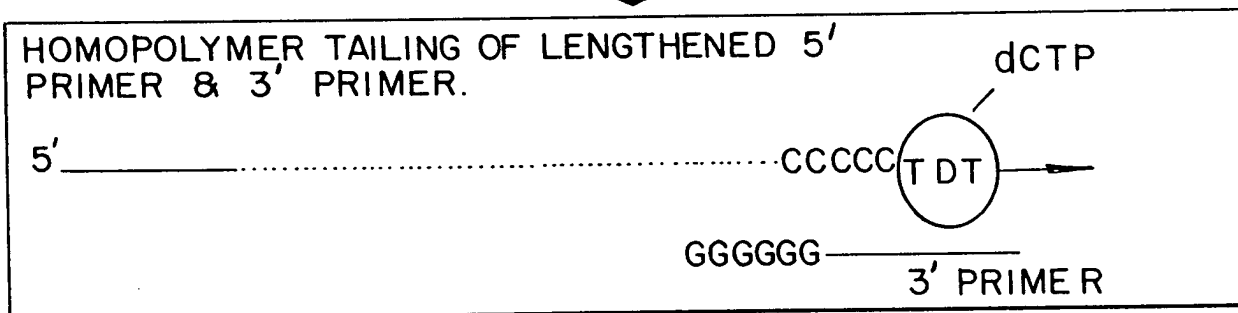
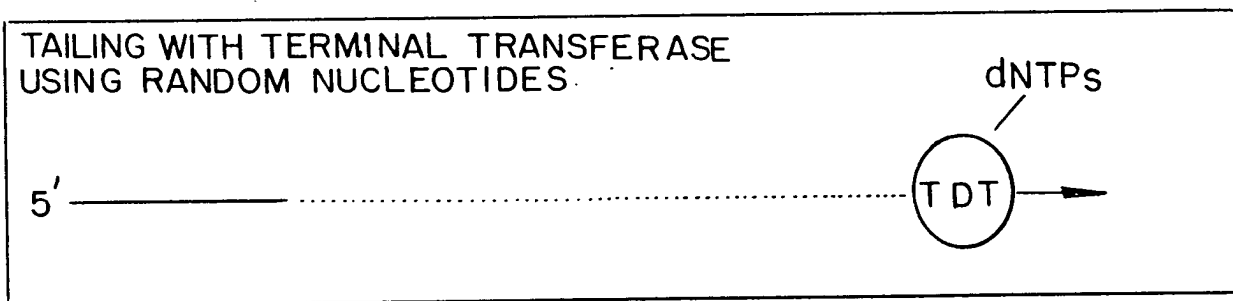


FIG. 8



"WALKING" BY EXTENDING THE PRIMARY LIGAND.

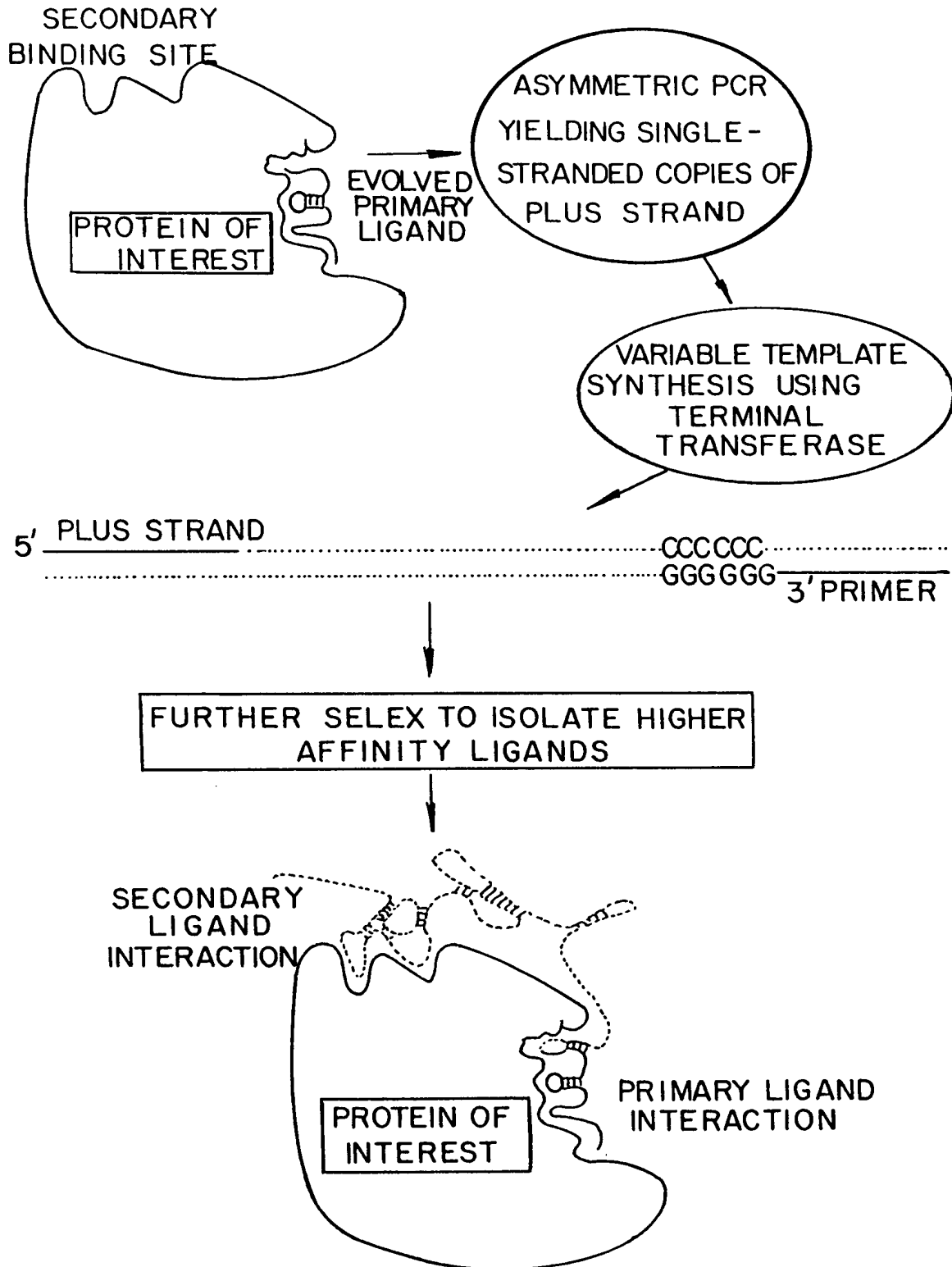
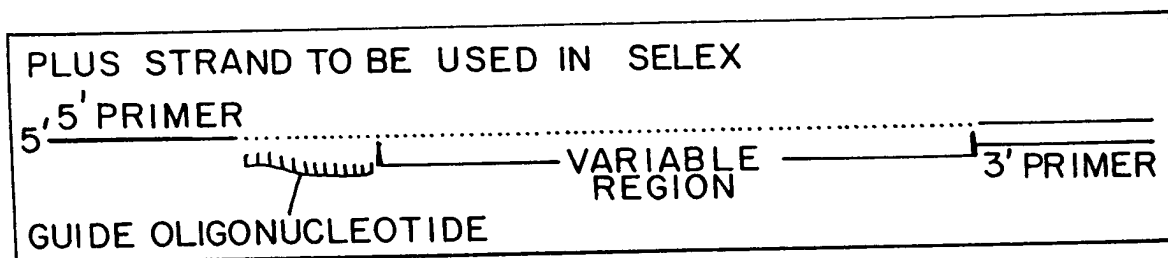
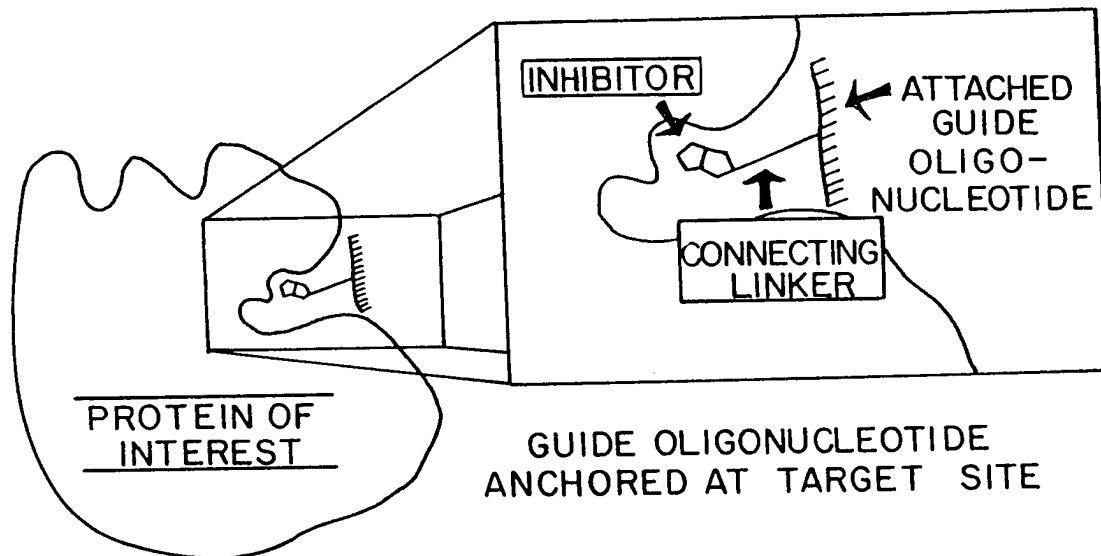


FIG.9

10037986-1080  
FOR OFFICIAL USE ONLY

ANCHORING OF BRIDGING OLIGONUCLEOTIDE &  
SECONDARY LIGAND EVOLUTION.



SELEX LEADS TO ISOLATION OF LIGANDS THAT INTERACT WITH SECONDARY BINDING SITES

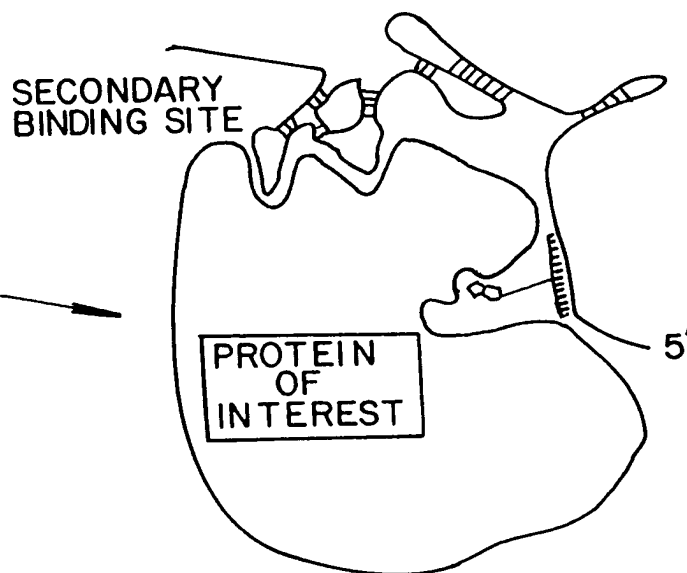


FIG.10

SECONDARY LIGAND-DIRECTED PRIMARY LIGAND EVOLUTION.

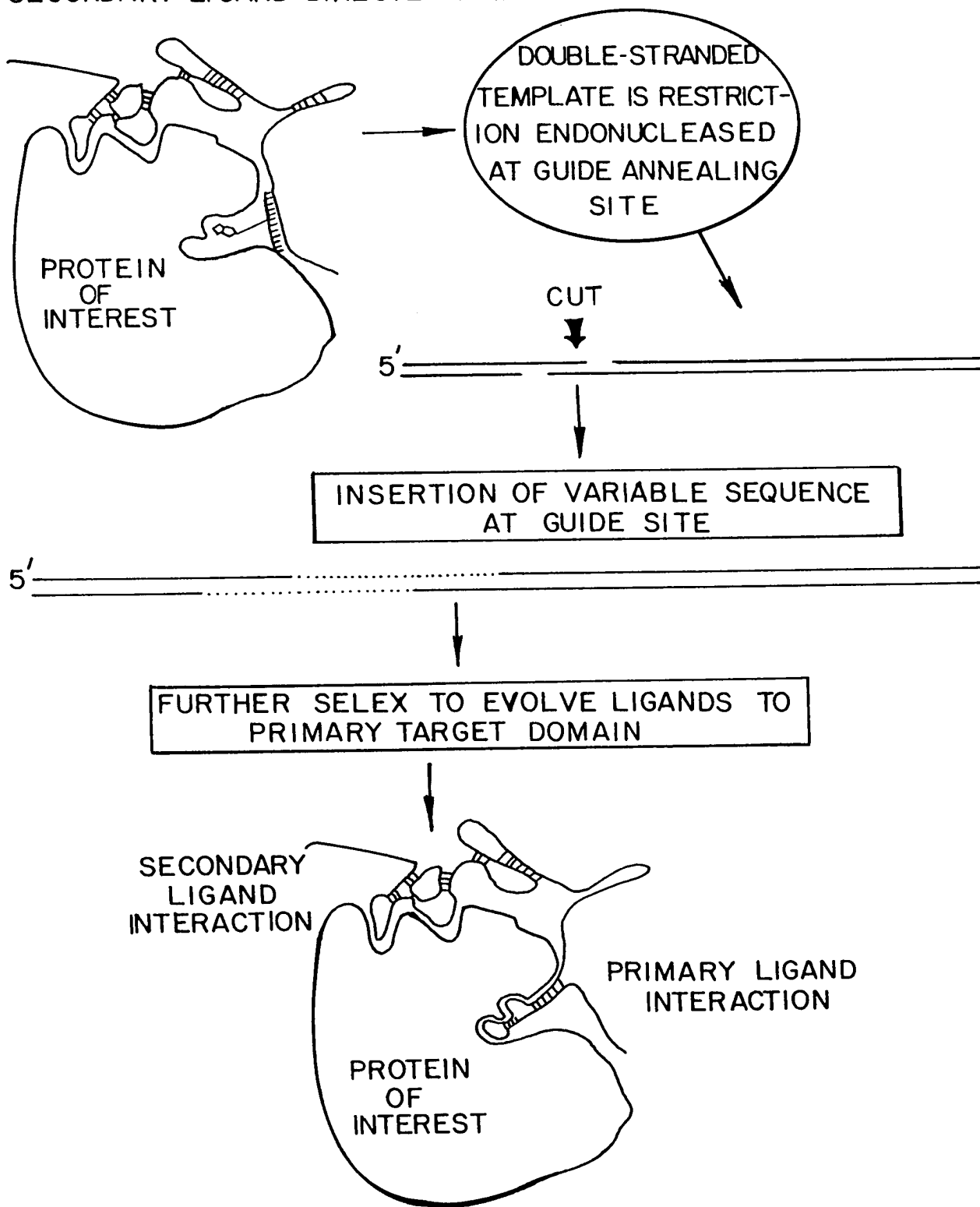


FIG.11

1003967001

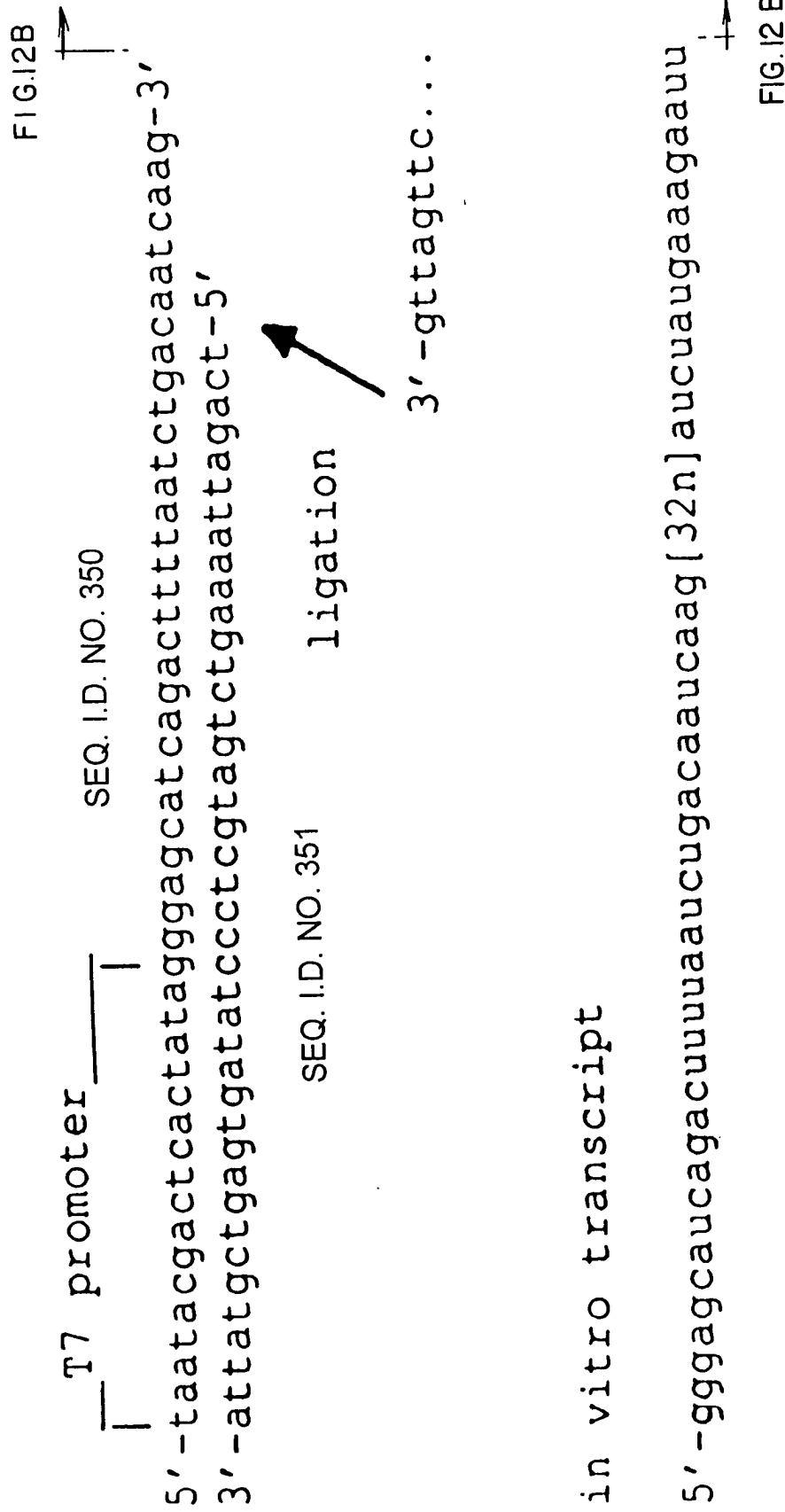


FIG. 12B

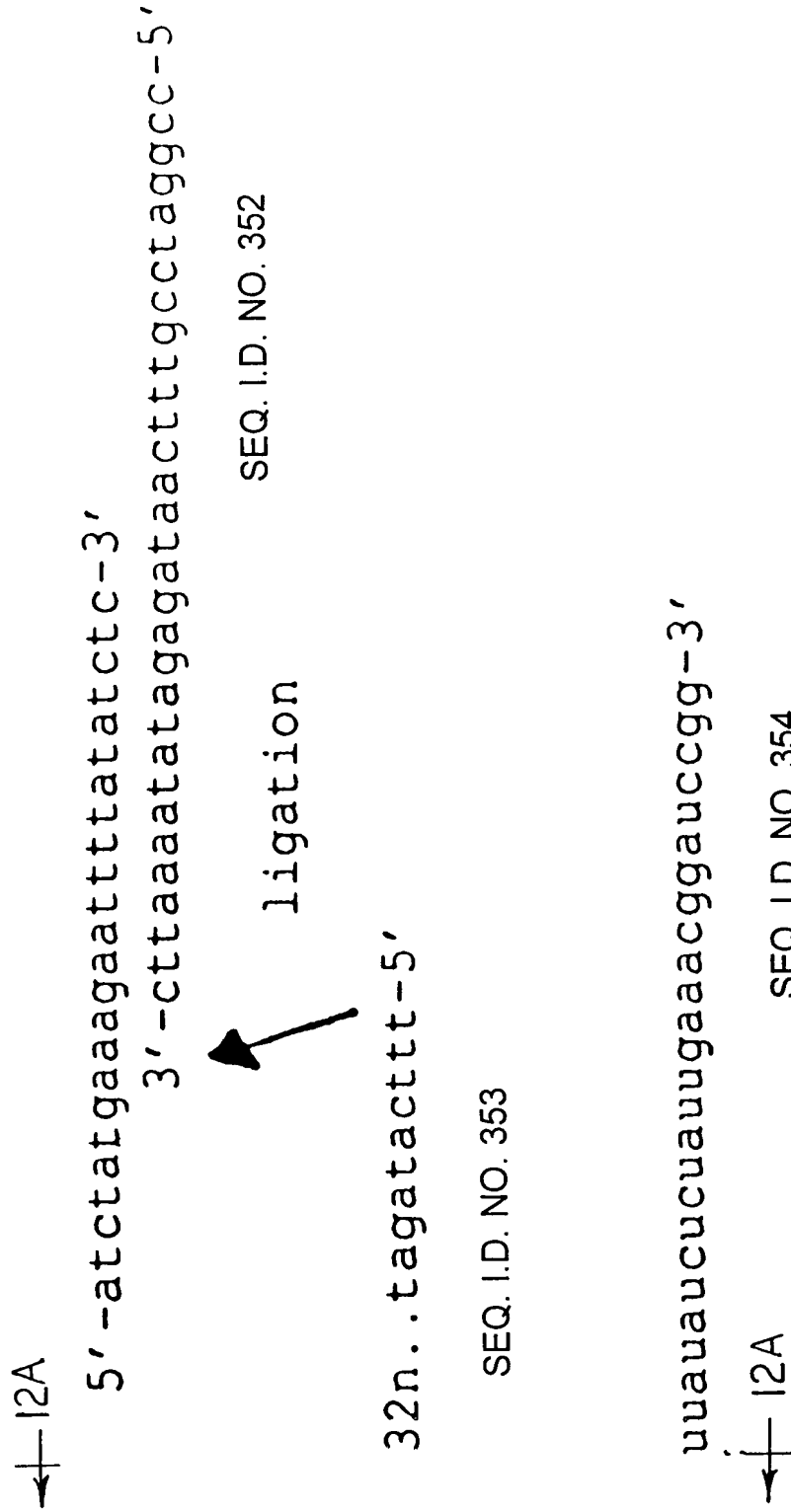


FIG. 12B

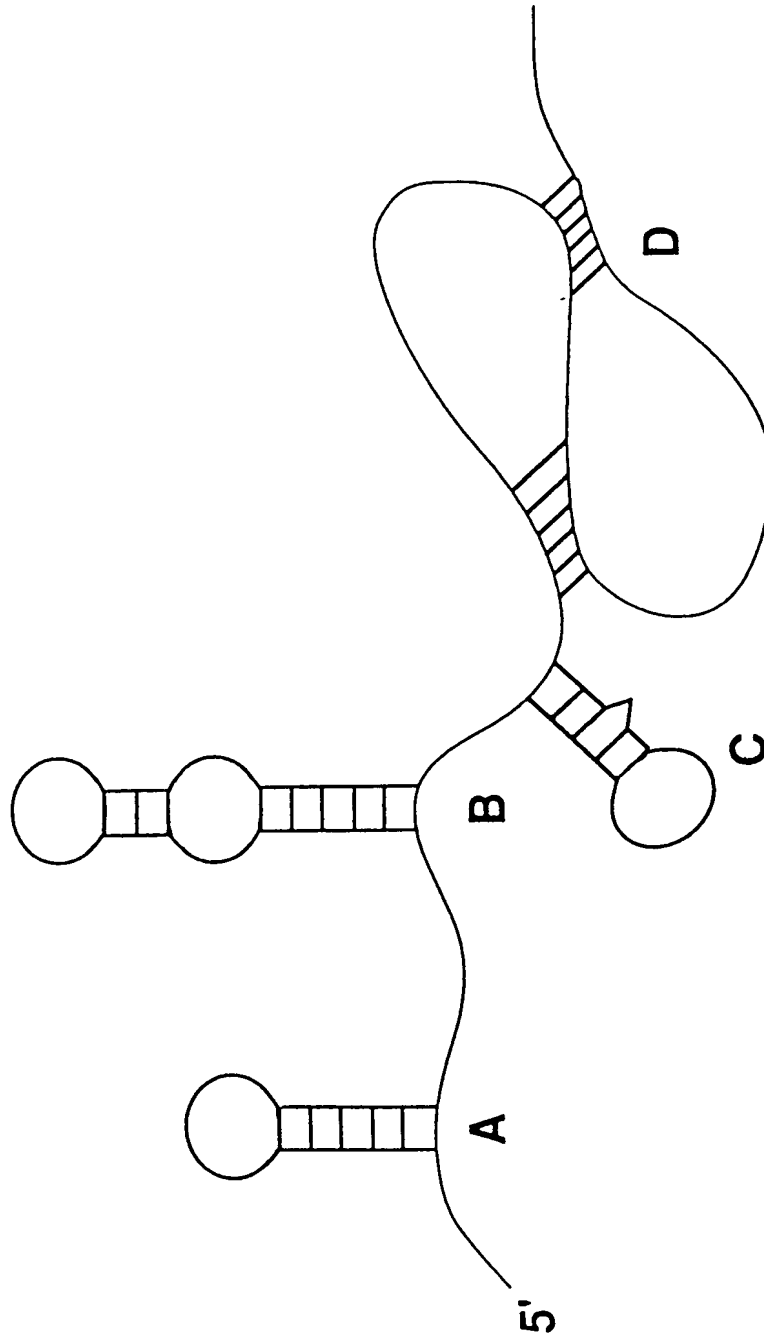
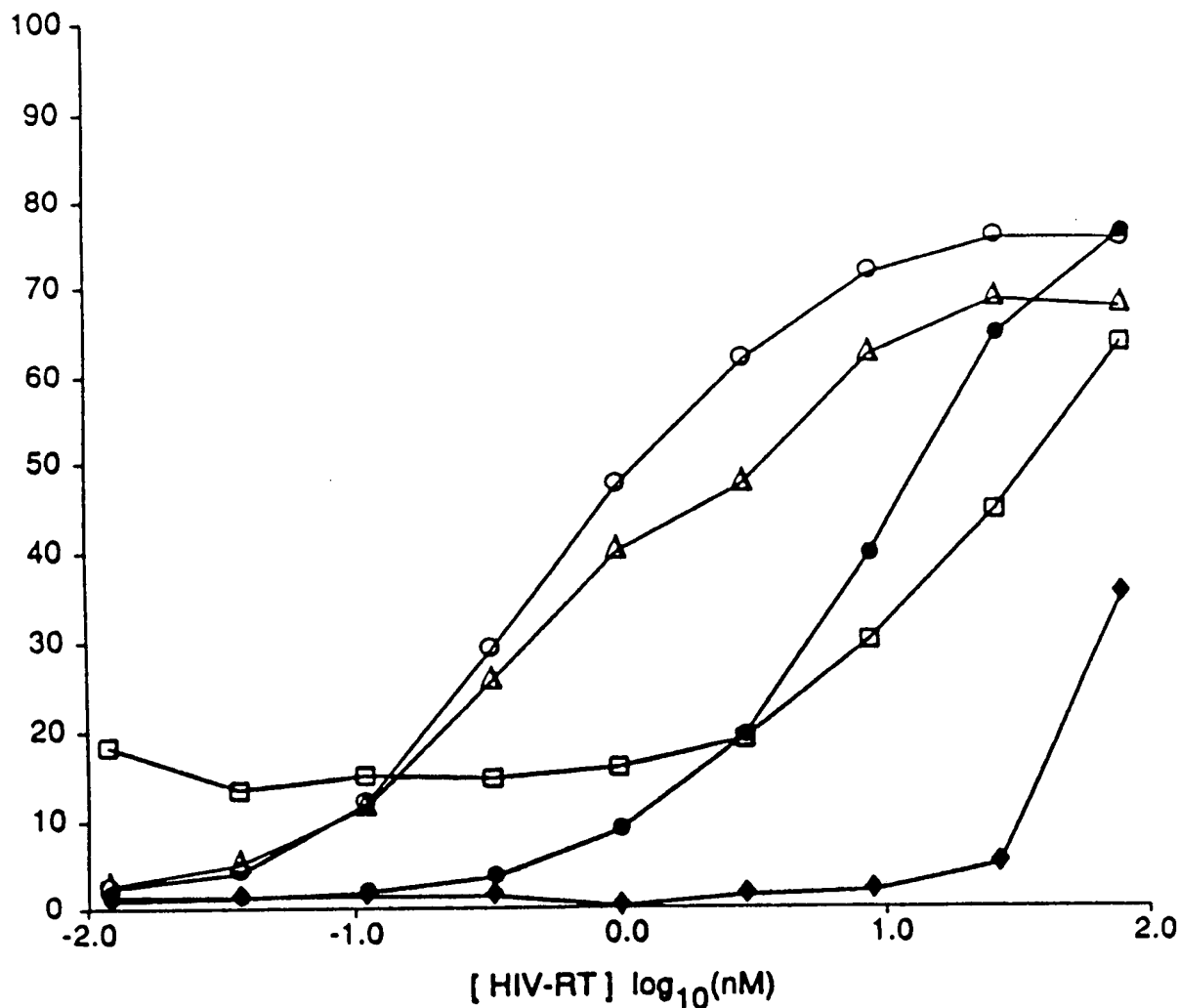


FIG.13

FIG.14



Δ 1.1 ucaagAAUUCCGUUUUCAGUCGGGAAAAACUGAACA ducu (13)

○ 1.3 ucaagAAUAUCUUCCGAAGCCGAACGGGAAAACCGG'Caucu (1)

● 1.3 -----G-----A----- (1)

□ 1.4 ucaagGGCAUCUGGGAGGGUAAGGGUAAGGUUGUCGGaucu (4)

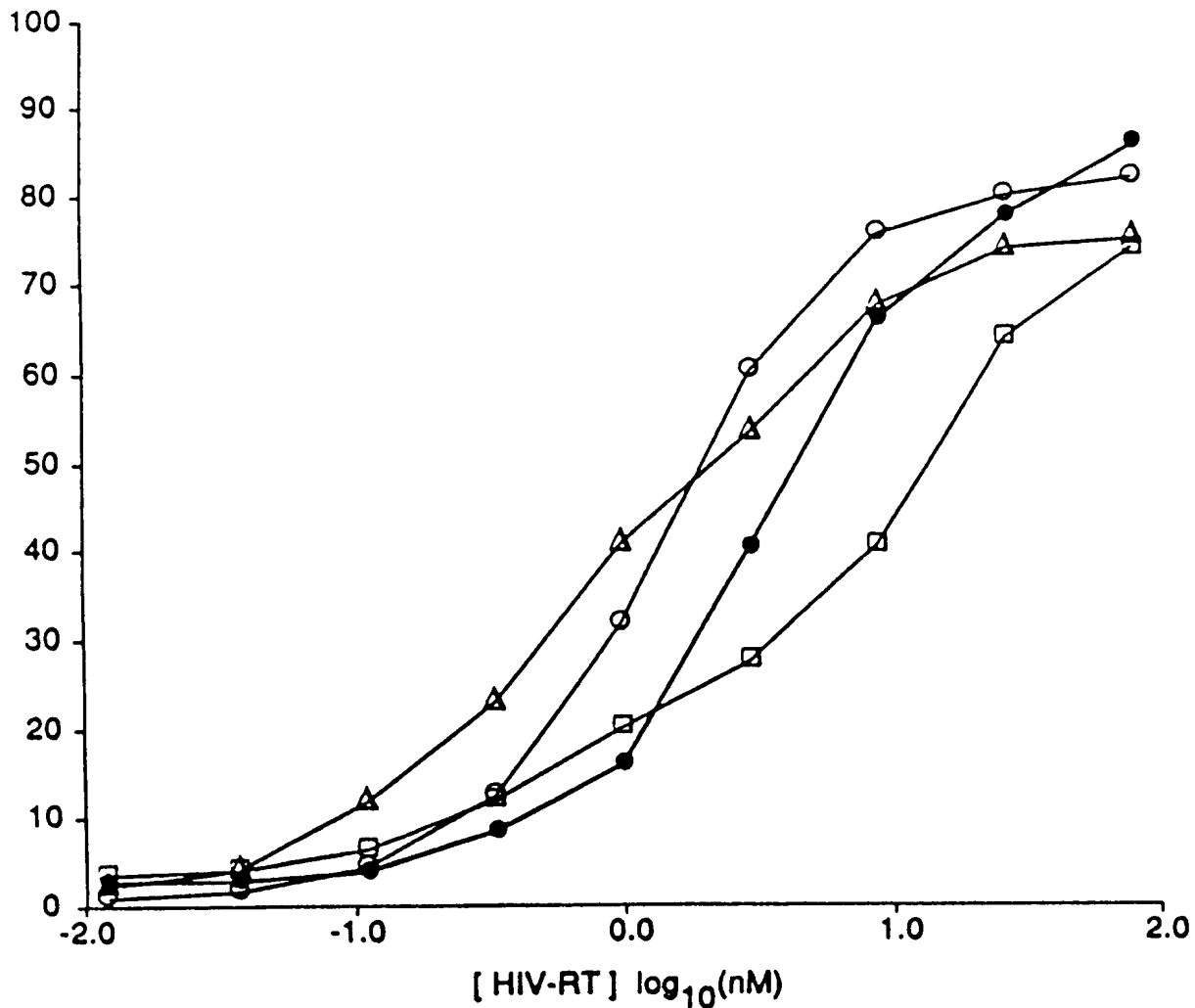
Δ 1.1 = SEQ. I.D. NO. 355

● 1.3 = SEQ. I.D. NO. 357

○ 1.3 = SEQ. I.D. NO. 356

□ 1.4 = SEQ. I.D. NO. 358

FIG.15



ISOLATE

○ 2.1a ucaag--AAUAUA-UCCGAACUCGACGGGAUAACGAGAA-Gaucu (3)

□ 2.2b ucaagUACCUAGGUGAUAAAAGGGAGAACACGUGUGa-cu (13)

● 2.5b ucaagACAGUAUCCGUUCUUGAUCAUCGGGACAAAUGaucu (3)

△ 1.1 ucaagAAUUCCGUUUUCAGUCGGGAAAAACUGAACAAUcu (13)

○ 2.1a = SEQ. I.D. NO. 359

● 2.5b = SEQ. I.D. NO. 361

□ 2.2b = SEQ. I.D. NO. 360

△ 1.1 = SEQ. I.D. NO. 362



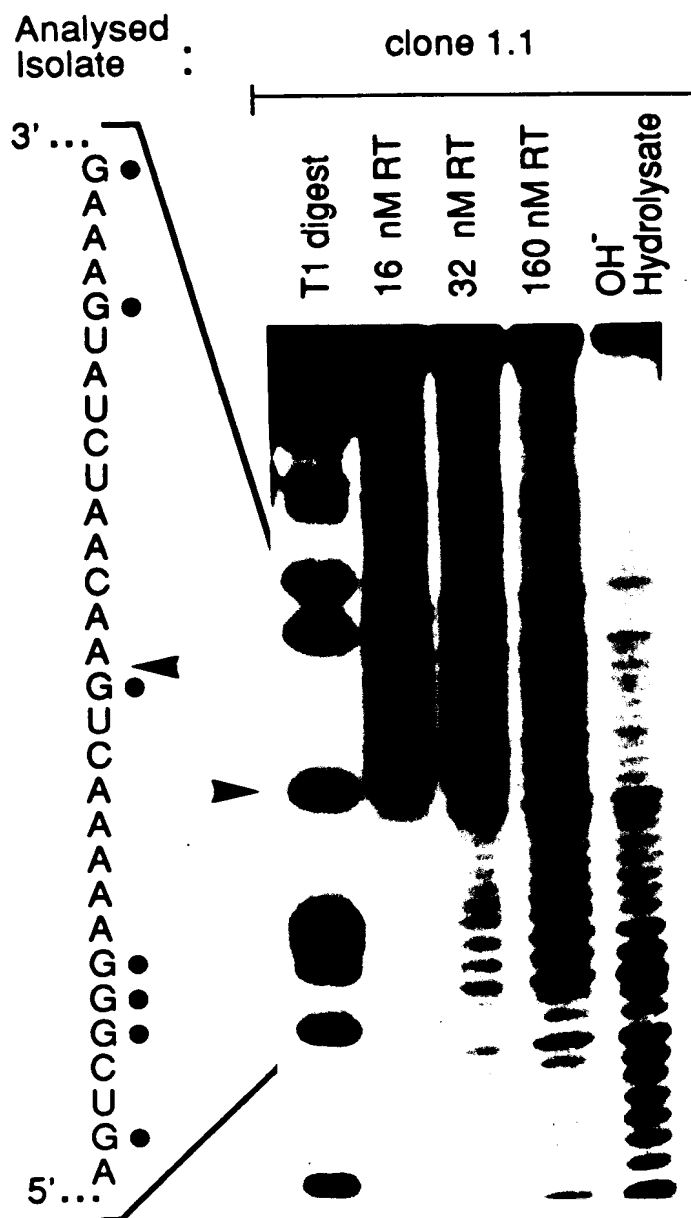


FIG. 16 A

SEQ. I.D. NO. 363

108101 985/E007

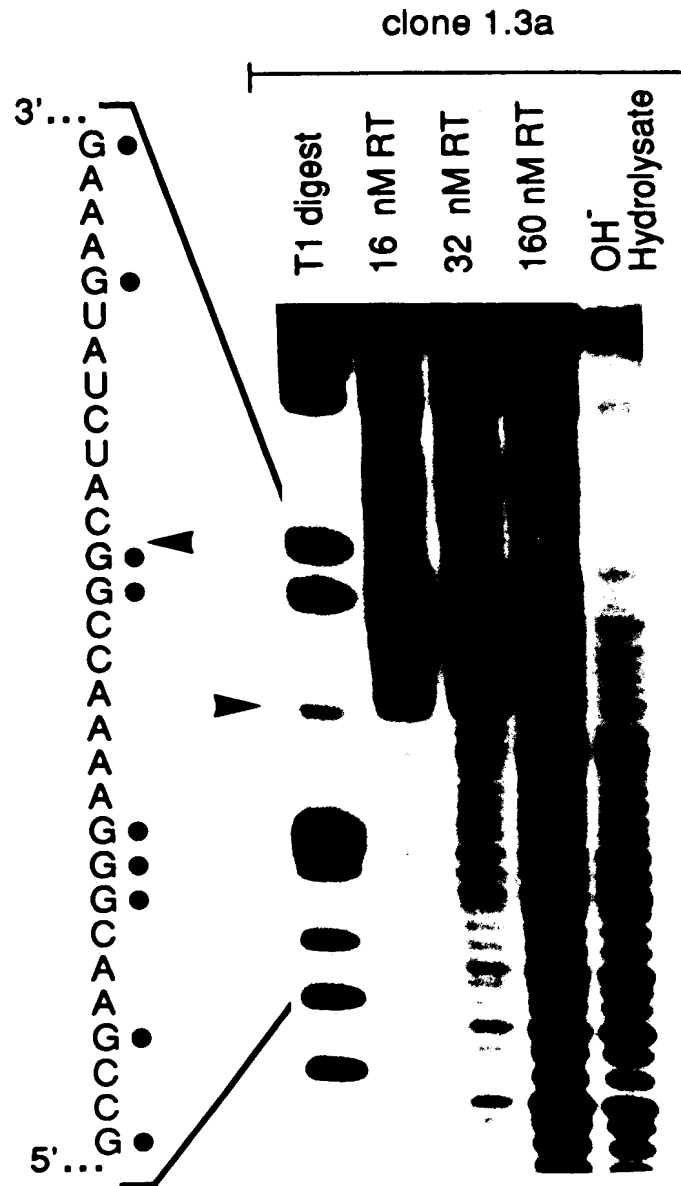
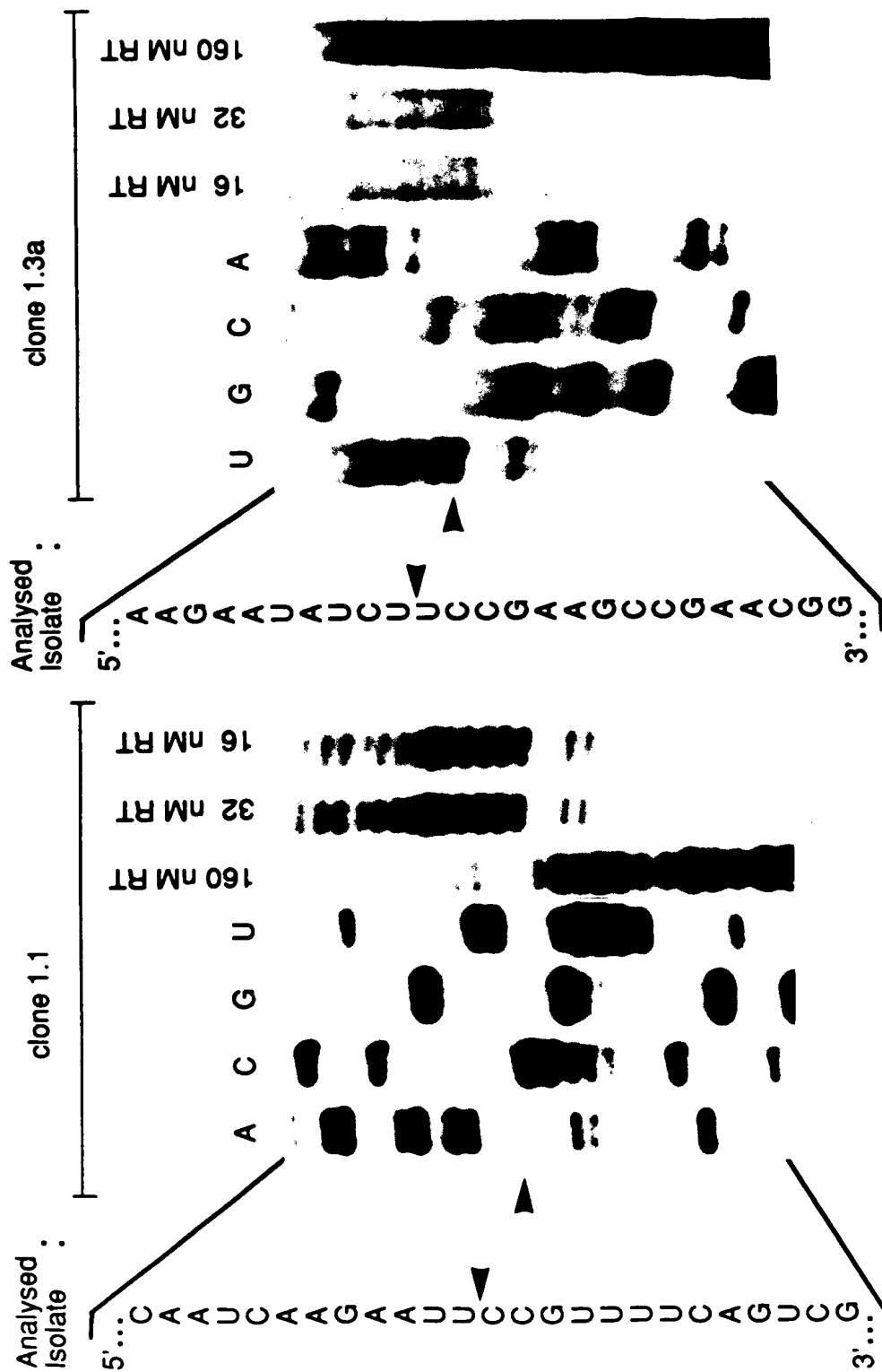


FIG.16 B

SEQ. I.D. NO. 364

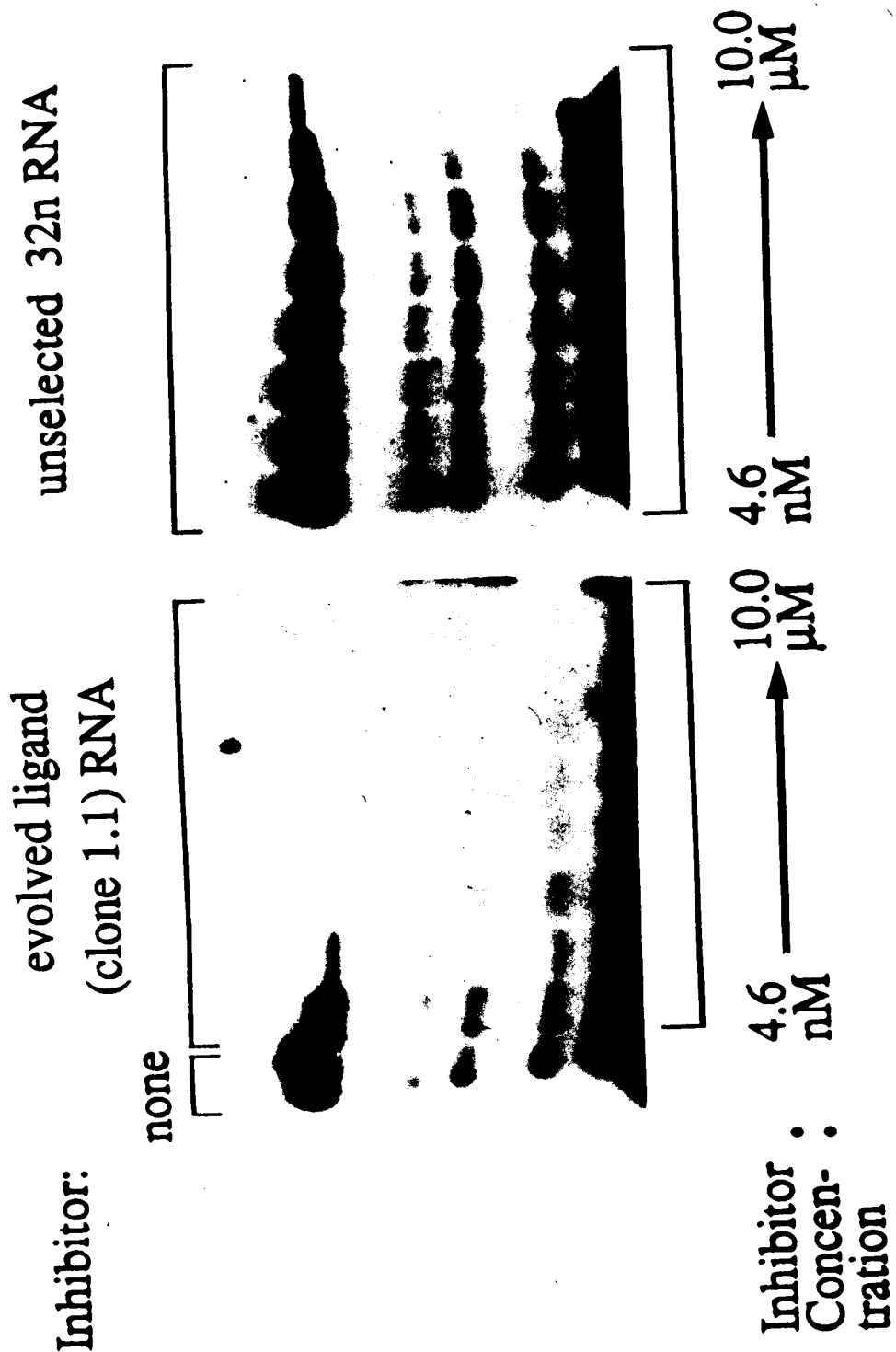
FIG.16 C



SEQ. I.D. NO. 366

SEQ. I.D. NO. 365

FIG. 17B



Reverse Transcriptase : Species	AMV	MMLV	HIV-1
Inhibitor :	evolved ligand (clone 1.1) RNA	evolved ligand (clone 1.1) RNA	evolved ligand (clone 1.1) RNA
Inhibitor Concentration : (nM)	0, 4, 20, 100, 500	0, 4, 20, 100, 500	0, 4, 20, 100, 500
	32n RNA	32n RNA	32n RNA

FIG.19B

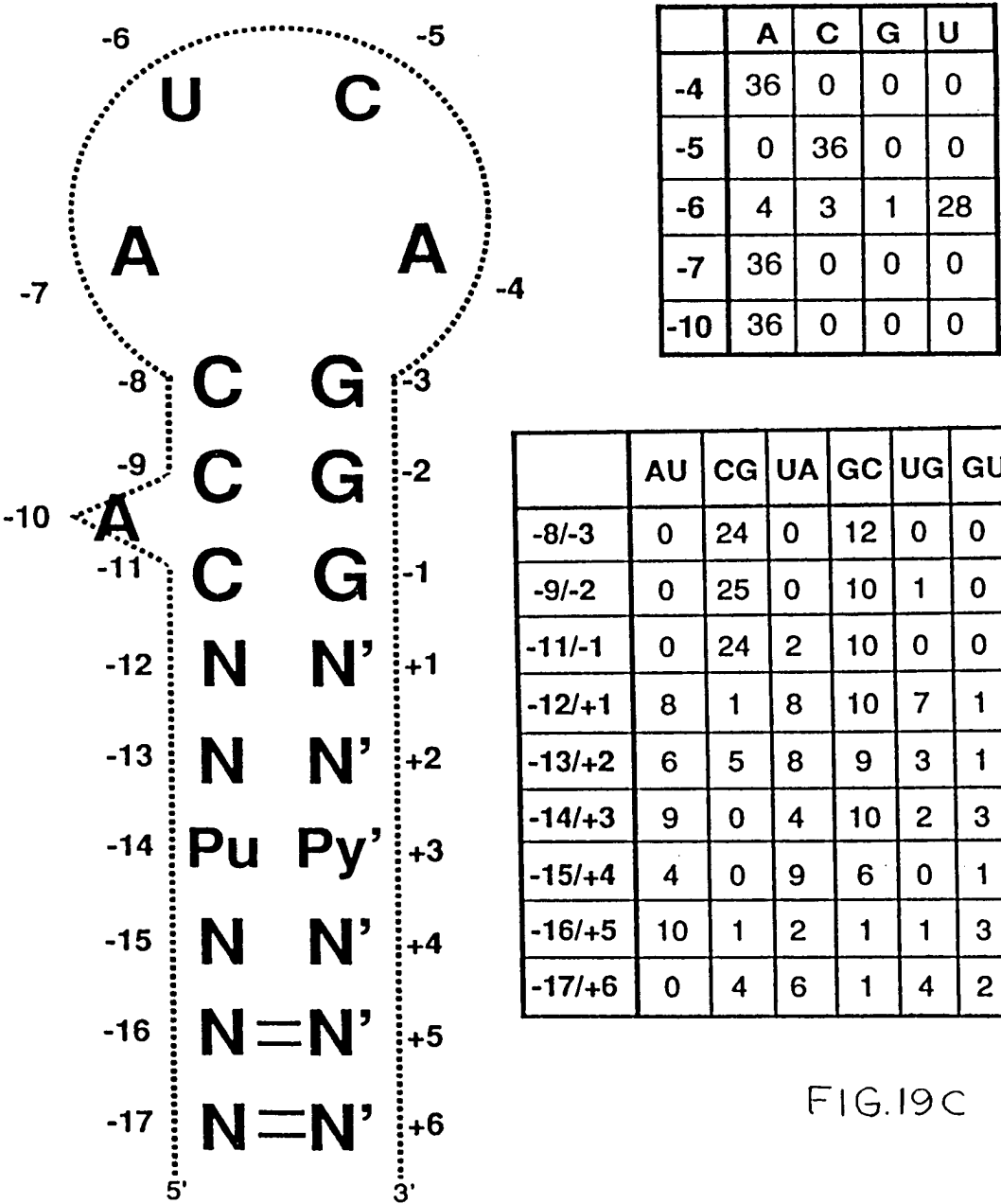


FIG.19A

SEQ. I.D. NO. 367

FIG.20

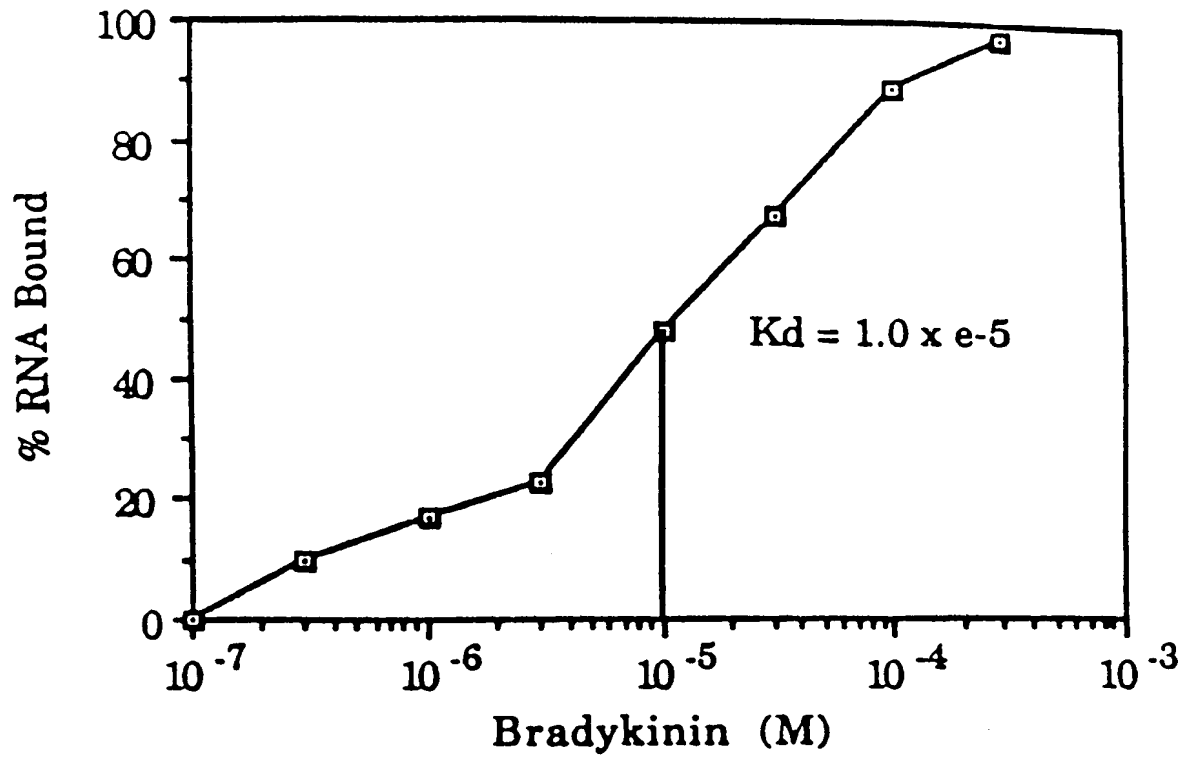


FIG.21A

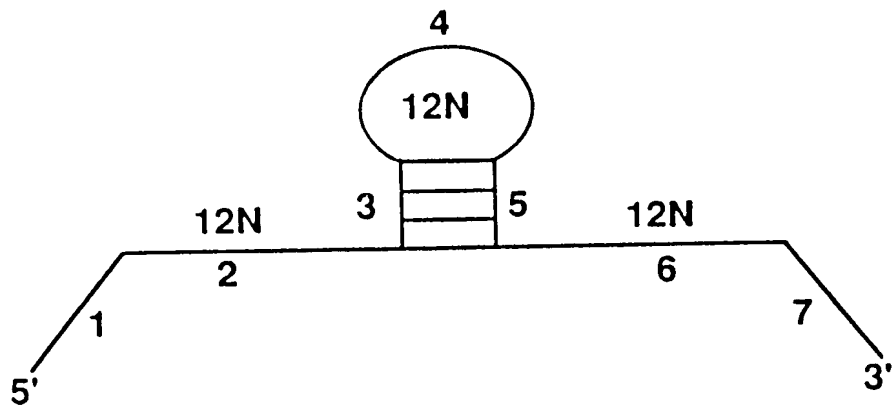
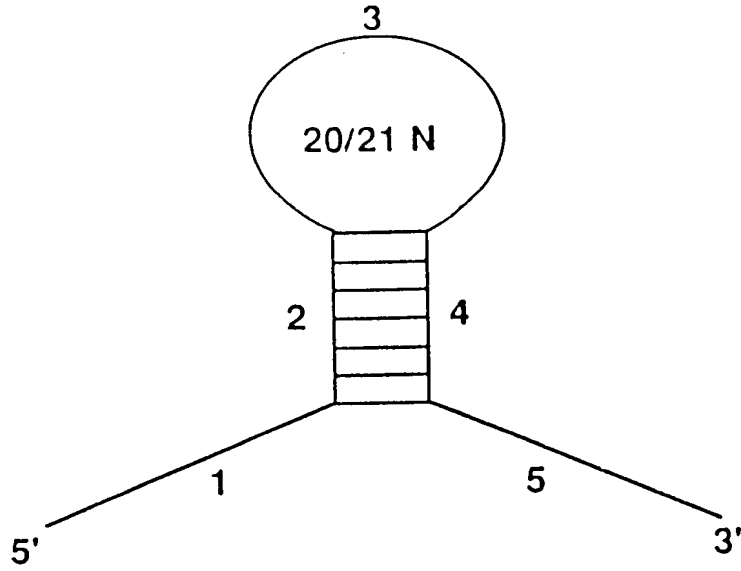


FIG.21B

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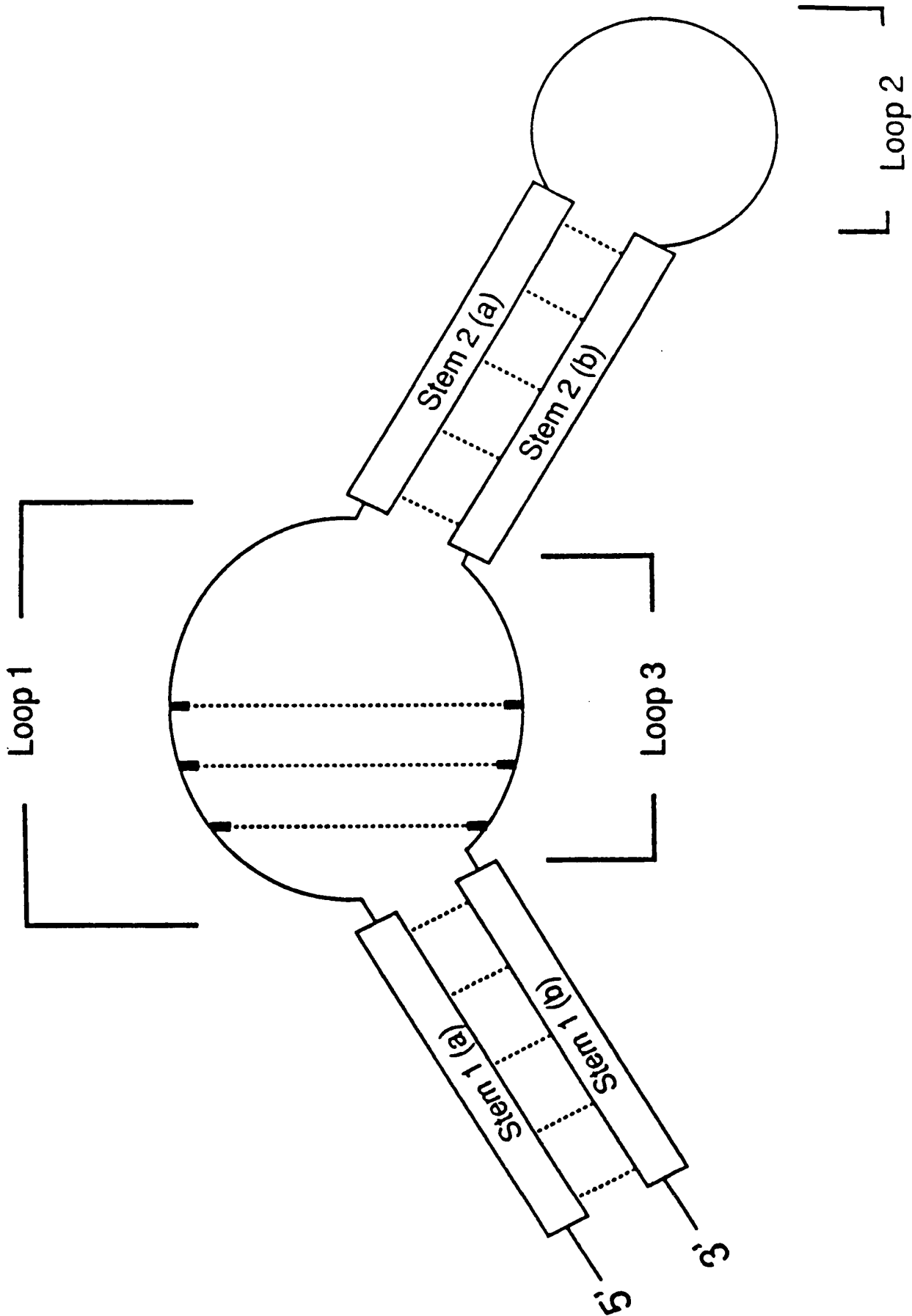


FIG.22

10037986-10101

FOOTNOTES

Motif I (6a)

UUGAGAAA G  
 5' ... gGGUGCA ||| CAC U (NUCLEOTIDES 2-38 OF SEQ. I.D. NO. 301)  
 3' ... ucuaUGU ||| GUG U  
 --CUCA-G U

Motif III (9a)

CC UUGaucua-  
 A GG ||||| uga-3'  
 A CC ||||| GCUU-5'  
 UU --CUAGUAA

Motif II (1c)

AAGAUU UCU  
 5' ... AGAUG CAGC  
 3' ... ucuAC GUCC A  
 -ACA-G UAG

SEQ. I.D. NO. 369

SEQ. I.D. NO. 368

WT (Motif II-like Domain)

U ACGGUA  
 A GACGCUG || CA...3'  
 CUGCGAC || GU...5'  
 A -GCG-G

SEQ. I.D. NO. 370

FIG. 23

FIG. 24

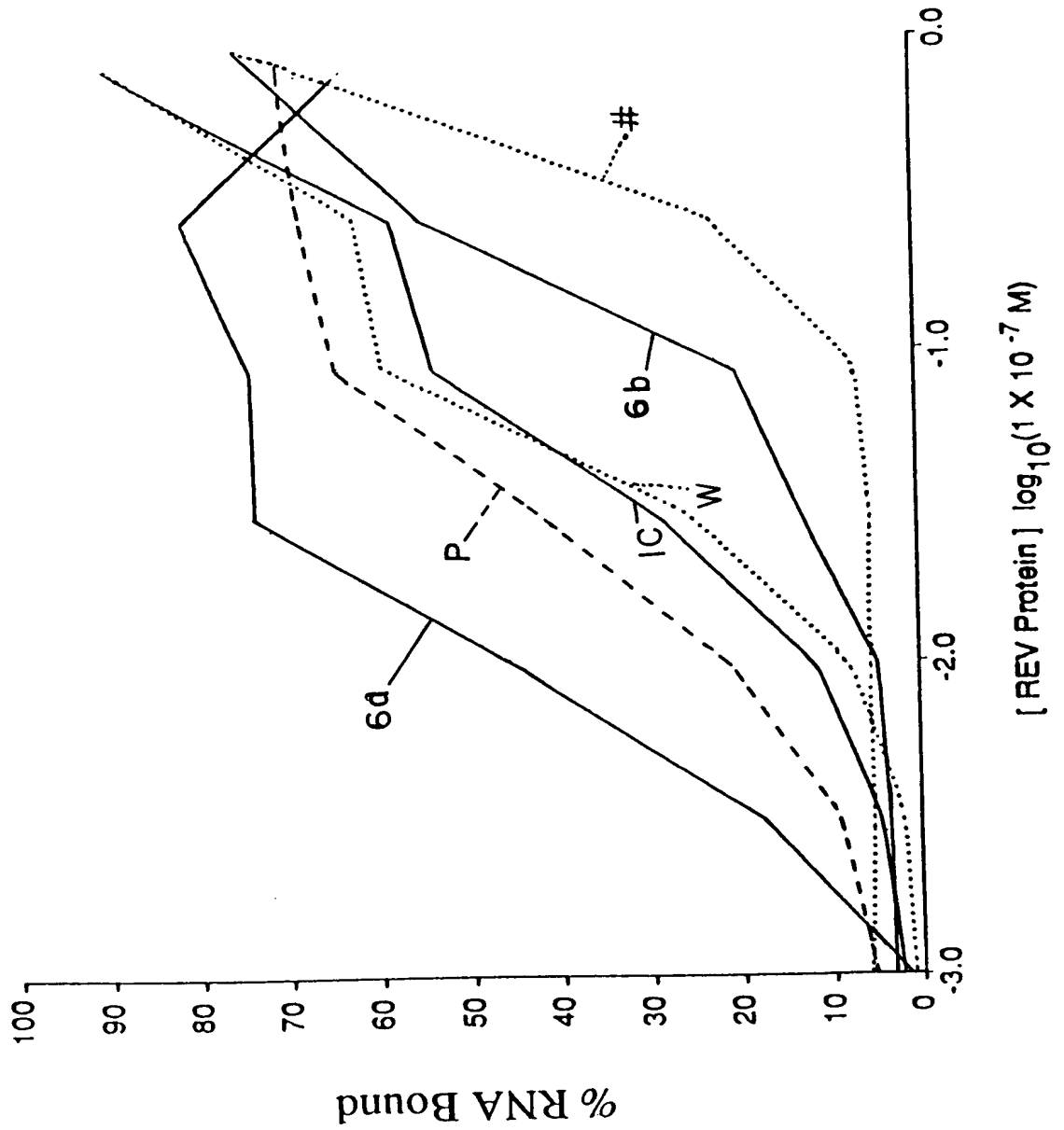


FIG. 25

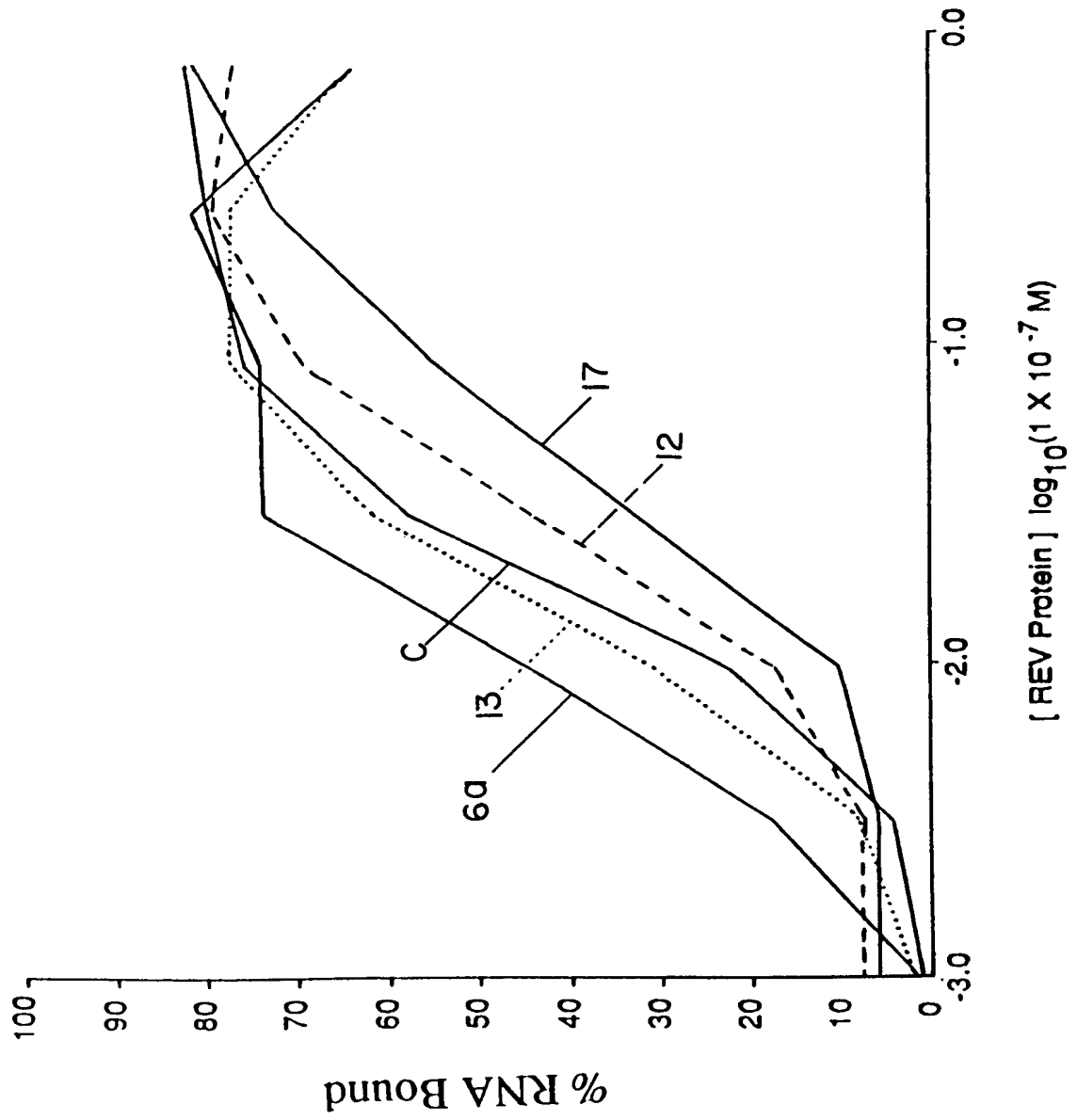
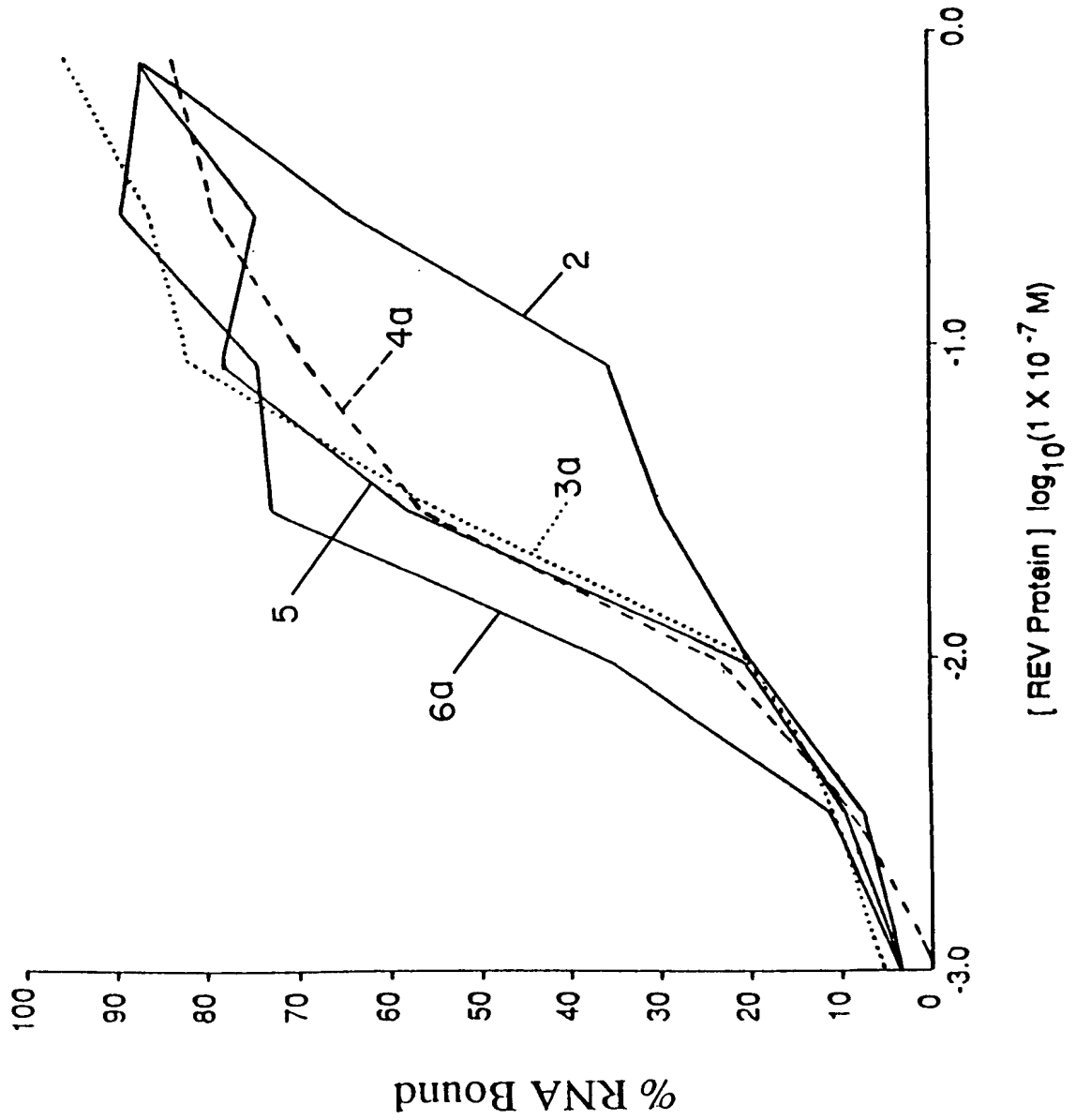


FIG.26



FOOT" 9862E00T

FIG.27

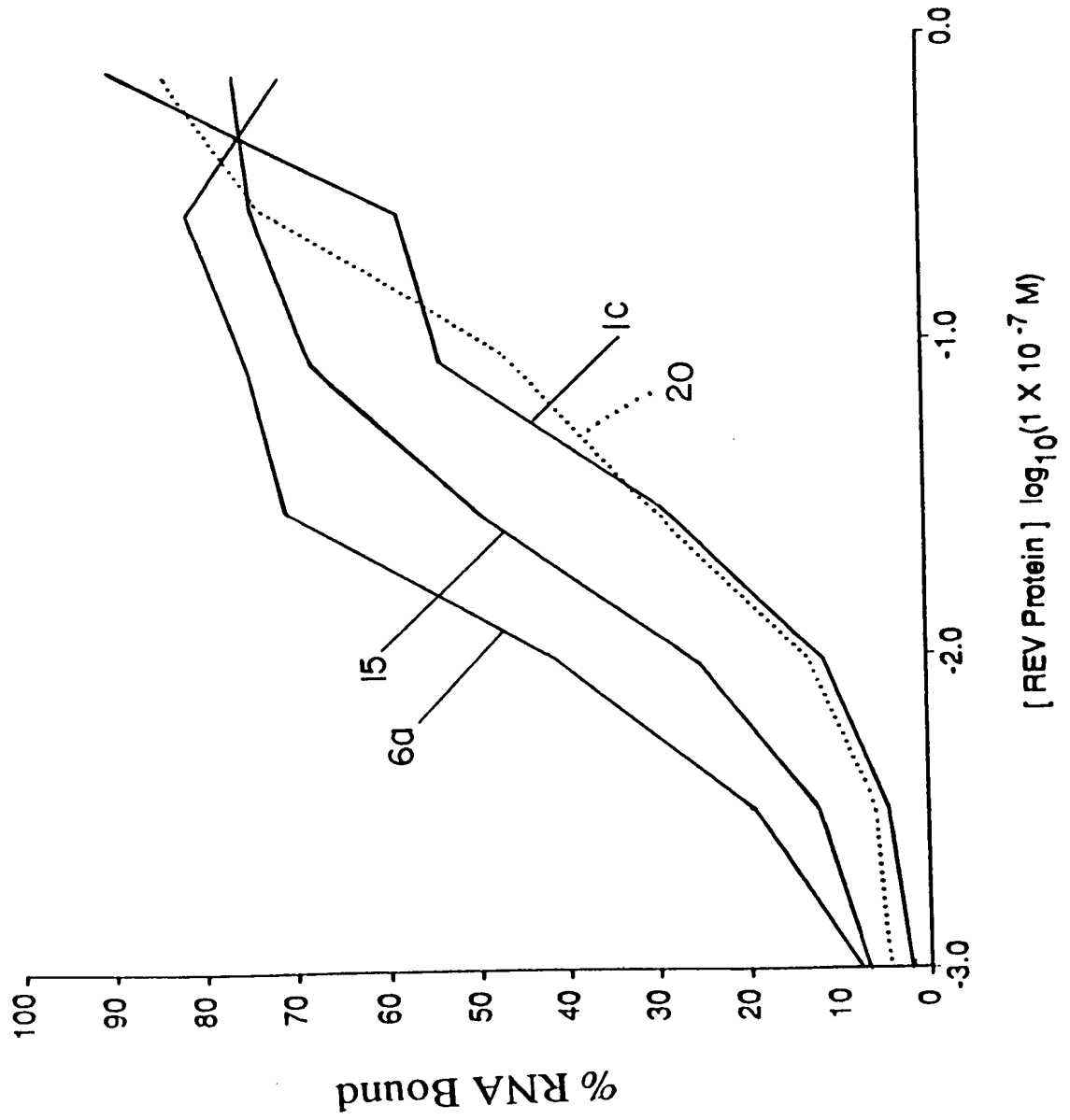
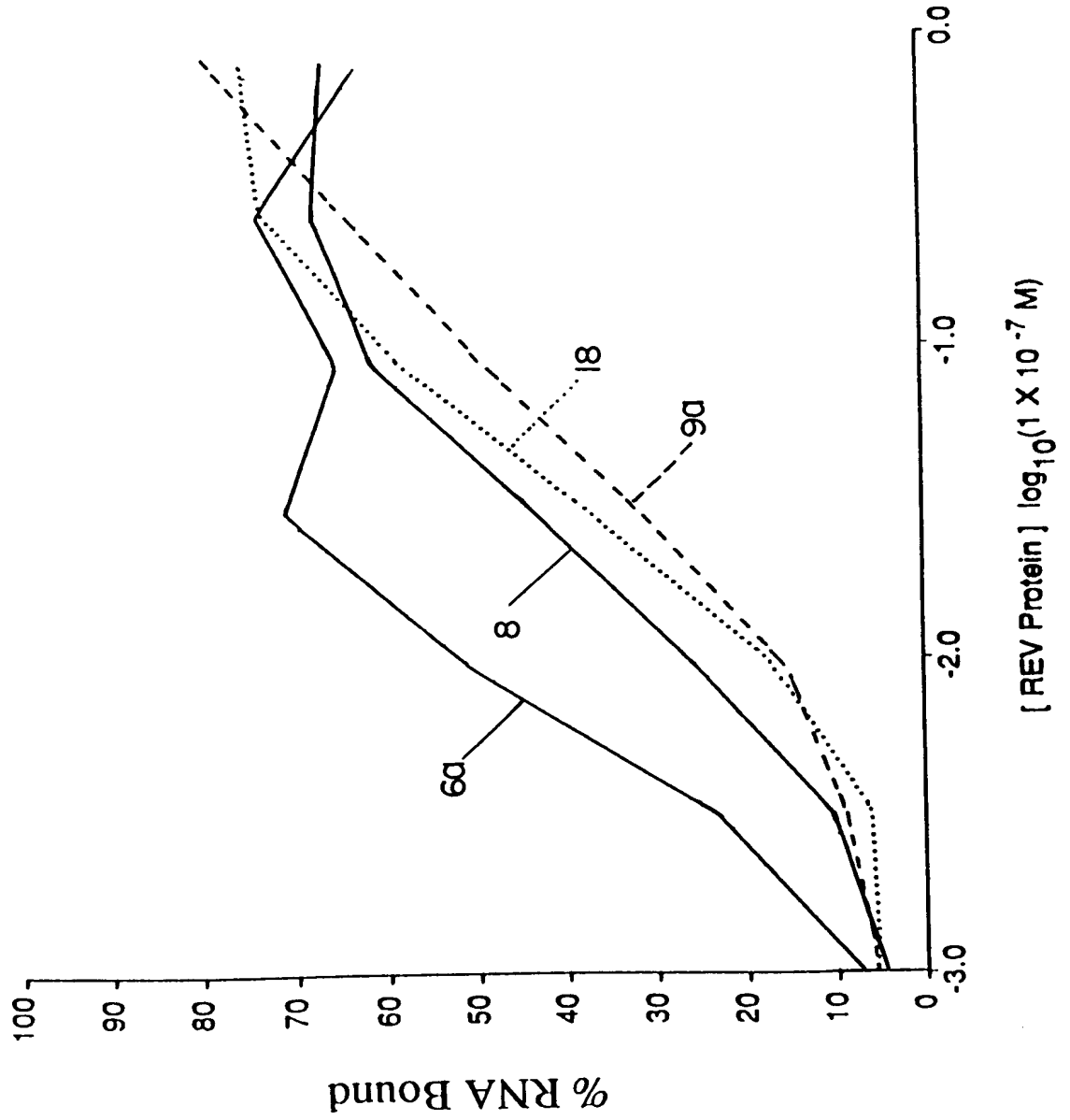


FIG. 28



100395 10101

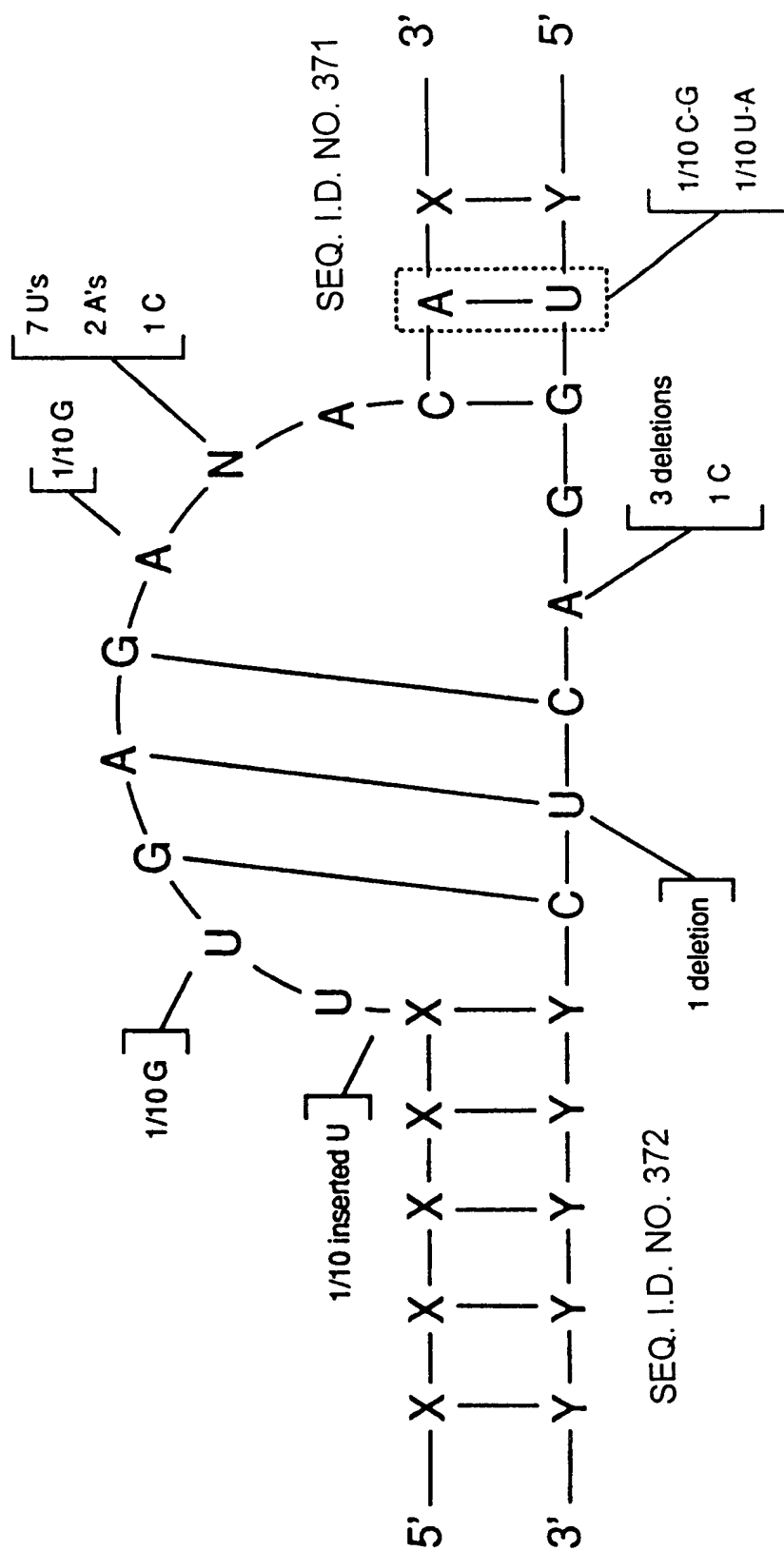
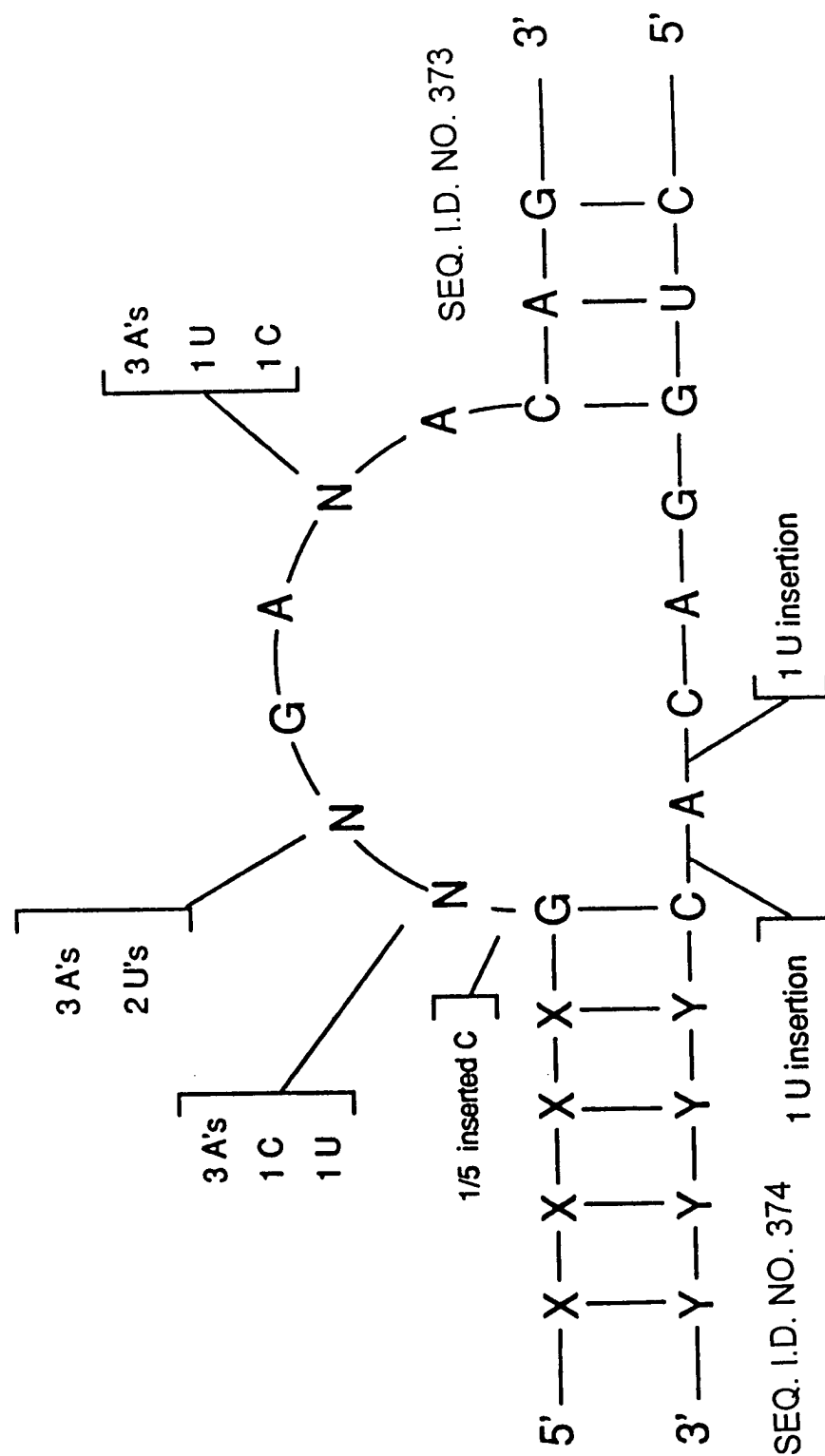


FIG. 29



FIG. 30



## Motif II

FIG. 3I

